

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 16:54:56 ; Search time 118.5 Seconds
(without alignments)
1019.010 Million cell updates/sec

Title: US-10-600-997-6

Perfect score: 1552

Sequence: 1 MKTLPAMLTGKLFVWFPLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap:
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap:
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap:
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap:
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap:
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	100.0	289	4	US-10-371-341-2
2	1552	100.0	289	4	US-10-600-997-6
3	1552	100.0	289	5	US-10-831-622-21
4	1552	100.0	289	5	US-10-964-215-21
5	1552	100.0	289	5	US-10-989-826-28
6	1552	100.0	521	5	US-10-831-622-98
7	1552	100.0	521	5	US-10-964-215-98
8	1516	97.7	289	4	US-10-600-997-8
9	1383	89.1	259	5	US-10-831-622-20
10	1383	89.1	259	5	US-10-964-215-20
11	1282	82.6	239	5	US-10-831-622-19
12	1282	82.6	239	5	US-10-964-215-19
13	1256	80.9	241	4	US-10-471-449-10
14	980	63.1	178	5	US-10-831-622-15
15	980	63.1	178	5	US-10-964-215-15
16	860	55.4	157	5	US-10-831-622-13
17	860	55.4	157	5	US-10-964-215-13
18	811	52.3	148	5	US-10-831-622-14
19	811	52.3	148	5	US-10-964-215-14
20	745.5	48.0	212	4	US-10-062-548-88
21	745.5	48.0	212	5	US-10-918-446-88
22	745.5	48.0	212	6	US-11-002-755-88
23	745.5	48.0	212	6	US-11-002-756-88
24	743.5	47.9	306	4	US-10-600-997-5
25	743.5	47.9	306	4	US-10-600-997-10
26	739.5	47.6	306	5	US-10-831-622-63
27	739.5	47.6	306	5	US-10-964-215-63

28 739.5 47.6 538 5 US-10-831-622-99 Sequence 99, Appl
29 739.5 47.6 538 5 US-10-964-215-99 Sequence 99, Appl
30 692 44.6 132 5 US-10-831-622-18 Sequence 18, Appl
31 692 44.6 132 5 US-10-964-215-18 Sequence 18, Appl
32 691 44.5 127 5 US-10-831-622-12 Sequence 12, Appl
33 691 44.5 127 5 US-10-964-215-12 Sequence 12, Appl
34 673.5 43.4 277 5 US-10-831-622-62 Sequence 62, Appl
35 673.5 43.4 277 5 US-10-964-215-62 Sequence 62, Appl
36 635.5 40.9 250 5 US-10-831-622-61 Sequence 61, Appl
37 635.5 40.9 250 5 US-10-964-215-61 Sequence 61, Appl
38 572 36.9 111 5 US-10-831-622-17 Sequence 17, Appl
39 572 36.9 111 5 US-10-964-215-17 Sequence 17, Appl
40 516 33.2 102 4 US-10-062-548-107 Sequence 107, App
41 516 33.2 102 5 US-10-918-446-107 Sequence 107, App
42 516 33.2 102 6 US-11-002-755-107 Sequence 107, App
43 516 33.2 102 6 US-11-002-756-107 Sequence 107, App
44 474 30.5 204 5 US-10-831-622-57 Sequence 57, Appl
45 474 30.5 204 5 US-10-964-215-57 Sequence 57, Appl

ALIGNMENTS

RESULT 1

US-10-371-341-2

; Sequence 2, Application US/10371341

; Publication No. US20040091884A1

; GENERAL INFORMATION:

; APPLICANT: HILARY CLARK

; APPLICANT: DANIEL L. EATON

; APPLICANT: AUSTIN L. GURNEY

; APPLICANT: BERND WRANIK

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR THE TREATMENT OF

; FILE OF INVENTION: IMMUNE RELATED DISEASES

; FILE REFERENCE: P1996R1-US

; CURRENT APPLICATION NUMBER: US/10/371,341

; PRIOR FILING DATE: 2003-02-19

; PRIOR APPLICATION NUMBER: US 60/421,236

; NUMBER OF SEQ ID NOS: 2

; SEQ ID NO 2

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-371-341-2

Query Match 100.0%; Score 1552; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTLPAMLTGKLFVWFPLIPLYLDIWNTHGKSCDVLYIKROSEHSILAGDPFLECPV 60
Db 1 MKTLPAMLTGKLFVWFPLIPLYLDIWNTHGKSCDVLYIKROSEHSILAGDPFLECPV 60
QY 61 KYCANRPHVTWCKLANGTTCVKLEDRQTSWKBEKNISFFILHPEPVLPNDSYRCSANFQ 120
Db 61 KYCANRPHVTWCKLANGTTCVKLEDRQTSWKBEKNISFFILHPEPVLPNDSYRCSANFQ 120
QY 121 SNLISHSTTLVTVTVKASERPSKDEMASRPWLLYSLLPLGGLPLLIITTCFLCFLCLR 180
Db 121 SNLISHSTTLVTVTVKASERPSKDEMASRPWLLYSLLPLGGLPLLIITTCFLCFLCLR 180
QY 181 HOGKQNELSDTAGREINLVDAHLKSEQTEASTRONSOVLSETGYVNDPDLCPFRMQEGS 240
Db 181 HOGKQNELSDTAGREINLVDAHLKSEQTEASTRONSOVLSETGYVNDPDLCPFRMQEGS 240
QY 241 EYVSNPCLEENKPGIVYASLNHSVIGLNSRLARNVKEAPTEYASICVRS 289
Db 241 EYVSNPCLEENKPGIVYASLNHSVIGLNSRLARNVKEAPTEYASICVRS 289

RESULT 2

US-10-600-997-6

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; Sequence 6, Application US/10600997
; Publication No. US20040175380A1
; GENERAL INFORMATION:
; APPLICANT: Allison, James
; APPLICANT: Murphy, Kenneth
; APPLICANT: Watanabe, Norihiko
; APPLICANT: Murphy, Theresa
; APPLICANT: Yang, Jianfei
; APPLICANT: Zang, Xingxing
; TITLE OF INVENTION: Compositions and Methods for Modulating Lymphocyte Activity
; FILE REFERENCE: A-71608/TAL/DRH
; CURRENT APPLICATION NUMBER: US/10/600,997
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/390,653
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/438,593
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-997-6

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Query Match 100.0%; Score 1552; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P P F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P P F L E C P V 60

QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H F E P V L P N D N G S Y R C S A N F Q 120
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H F E P V L P N D N G S Y R C S A N F Q 120

QY 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L L Y S L L P L G L P L L I T T C F C L F C C L R R 180
D b 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L L Y S L L P L G L P L L I T T C F C L F C C L R R 180

QY 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240
D b 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240

QY 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289
D b 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289

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RESULT 3
US-10-831-622-21
; Sequence 21, Application US/10831622
; Publication No. US20040248257A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Jonathan
; APPLICANT: Wilkinson, Beverley
; TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: TSRI 810.1
; CURRENT APPLICATION NUMBER: US/10/831,622
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-831-622-21

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Query Match 100.0%; Score 1552; DB 5; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;

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Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P P F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P P F L E C P V 60

QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H F E P V L P N D N G S Y R C S A N F Q 120
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H F E P V L P N D N G S Y R C S A N F Q 120

QY 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L L Y S L L P L G L P L L I T T C F C L F C C L R R 180
D b 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L L Y S L L P L G L P L L I T T C F C L F C C L R R 180

QY 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240
D b 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240

QY 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289
D b 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289

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RESULT 4
US-10-964-215-21
; Sequence 21, Application US/10964215
; Publication No. US20050152893A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Jonathan
; TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION
; FILE REFERENCE: TSRI 810.2
; CURRENT APPLICATION NUMBER: US/10/964,215
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/831,622
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-964-215-21

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Query Match 100.0%; Score 1552; DB 5; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P P F L E C P V 60
D b 1 M K T L P A M L G T G K L F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S H S I L A G D P P F L E C P V 60

QY 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H F E P V L P N D N G S Y R C S A N F Q 120
D b 61 K Y C A N R P H V T W C K L N G T T C V K L E D R Q T S W K E E K N I S F F I L H F E P V L P N D N G S Y R C S A N F Q 120

QY 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L L Y S L L P L G L P L L I T T C F C L F C C L R R 180
D b 121 S N L I E S H S T T L Y V T D V K S A S E R P S K D E M A S R P W L L Y S L L P L G L P L L I T T C F C L F C C L R R 180

QY 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240
D b 181 H O G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S 240

QY 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289
D b 241 E V Y S N P C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P T E Y A S I C V R S 289

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RESULT 5
US-10-989-826-28

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 16:43:11 ; Search time 143 Seconds
(without alignments)
887.975 Million cell updates/sec

Title: US-10-600-997-6
Perfect score: 1552
Sequence: 1 MKTLPMLGTGKLFWFVFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1552	100.0	289	8 ADH34661	Adh34661 Human BTL
2	1552	100.0	289	8 ADO43716	Ado43716 Amino aci
3	1552	100.0	289	8 ADU51070	Adu51070 Human spl
4	1552	100.0	289	8 ADV34145	Adv34145 Human BTL
5	1552	100.0	289	9 AEA23330	Aea23330 Tumor ant
6	1552	100.0	521	8 ADU51147	Adu51147 Spleen-ex
7	1545	99.5	289	8 ADH74500	Adh74500 Human mcd
8	1516	97.7	289	8 ADH34662	Adh34662 Human BTL
9	1515	97.6	283	8 ADH74498	Adh74498 Human mcd
10	1383	89.1	259	8 ADU51069	Adu51069 Human spl
11	1282	82.6	239	8 ADU51068	Adu51068 Human SPE
12	1256	80.9	241	5 ABG96272	Abg96272 Human imm
13	1256	80.9	241	8 ADV34146	Adv34146 Sequence
14	998	64.3	194	9 ADY19218	Ady19218 PRO polyp
15	980	63.1	178	8 ADU51064	Adu51064 Human SPE
16	860	55.4	157	8 ADU51062	Adu51062 Human SPE
17	830	53.5	390	8 ADV34147	Adv34147 Surface I
18	811	52.3	148	8 ADU51063	Adu51063 Human SPE
19	745.5	48.0	212	2 AAY30839	Aay30839 Human sec
20	745.5	48.0	212	6 ADA57288	Ada57288 Human sec
21	745.5	48.0	212	6 ADA41169	Ada41169 Human sec
22	743.5	47.9	306	8 ADH34664	Adh34664 Mouse BTL
23	739.5	47.6	306	8 ADU51112	Adu51112 Murine sp
24	739.5	47.6	538	8 ADU51148	Adu51148 Spleen-ex

25	692	44.6	132	8	ADU51067	Human SPE
26	691	44.5	127	8	ADU51061	Human SPE
27	673.5	43.4	277	8	ADU51111	Murine sp
28	635.5	40.9	250	8	ADU51110	Murine sp
29	572	36.9	111	8	ADU51066	Human spl
30	536	34.5	98	9	ABE92075	Human BTL
31	516	33.2	101	6	ADA57590	Human sec
32	516	33.2	101	6	ADA41487	Human sec
33	516	33.2	102	2	AAY30859	Human sec
34	474	30.5	204	8	ADU51106	Murine sp
35	440	28.4	78	3	AAO2951	Human sec
36	408	26.3	175	8	ADU51105	Murine sp
37	408	26.3	179	8	ADU51134	Murine sp
38	408	26.3	411	8	ADU51149	Spleen-ex
39	398.5	25.7	180	8	ADU51104	Murine sp
40	377	24.3	65	8	ADU51052	Human spl
41	355	22.9	67	8	ADU51055	Human SPE
42	342	22.0	150	8	ADU51135	Murine sp
43	341	22.0	126	8	ADU51109	Murine sp
44	332.5	21.4	151	8	ADU51103	Murine sp
45	265.5	17.1	102	8	ADU51108	Murine sp

ALIGNMENTS

RESULT 1

ADH34661

ID ADH34661 standard; protein; 289 AA.

XX ADH34661;

XX 11-MAR-2004 (first entry)

XX Human BTLA.

XX B7x; ligand; B and T lymphocyte attenuator; BTLA; tumour; inhibition;
tumour-specific; immunological tolerance; cancer; autoimmune disease;
diabetes; pre-eclampsia; rheumatoid arthritis; multiple sclerosis;
infection; graft rejection; cell cycle progression; differentiation;
survival; cytokine production; cytolytic activation;
antigen presentation; antibody production.

XX Homo sapiens.

PH Key Location/Qualifiers
FT Peptide 1..28
FT Disulfide-bond 58..115 /note= "Signal peptide"
FT Modified-site 110 /note= "Disulphide bond"
FT Domain 154..182 /note= "Glycosylated"
FT Region 223..229 /note= "Transmembrane domain"
FT Region 254..262 /note= "Conserved sequence"
FT Region 277..289 /note= "Conserved sequence"

WO2004000221-A2.

31-DEC-2003.

20-JUN-2003; 2003WO-US019614.

20-JUN-2002; 2002US-0390653P.

06-JAN-2003; 2003US-0438593P.

(REGC) UNIV CALIFORNIA.
(UNIW) UNIV WASHINGTON.

PI Allison JP, Murphy KP, Watanabe N, Murphy TL, Yang J, Zang X;
 DR WPI; 2004-082409/08.
 XX
 PT New recombinant B and T lymphocyte attenuator nucleic acid and protein,
 PT for modulating B and T lymphocyte activity, or for diagnosing and
 PT treating cancer, autoimmune disease or infectious disease.
 XX
 XX Example 4; Fig 19; 11pp; English.
 XX
 CC This sequence represents a human B and T lymphocyte attenuator (BTLA).
 CC BTLA acts as a negative regulator of both B and T lymphocyte activity,
 CC where signaling mediated by BTLA results in the inhibition of BTLA-
 CC positive lymphocyte activity. In BTLA-positive T cells BTLA signalling
 CC can inhibit TCR-induced T cell responses, such as cell cycle progression,
 CC differentiation, survival, cytokine production and cytolytic activation.
 CC In BTLA-positive B cells BTLA signalling can inhibit B cell antigen
 CC receptor-induced B cell responses, such as cell cycle progression,
 CC differentiation, survival, antigen presentation and antibody production.
 CC B7x is a ligand for the recombinant BTLA of the invention. B7x is able to
 CC negatively regulate B and T lymphocyte activity through its interaction
 CC with BTLA, which inhibits both B and T cell responses. Therefore B7x
 CC positive tumour tissue inhibits the activity of tumour-specific T cells.
 CC B7x is also expressed on non-tumour non-lymphoid tissue, showing that the
 CC B7x/BTLA interaction is a mechanism for maintaining immunological
 CC tolerance. BTLA proteins and related nucleic acids are useful for
 CC modulating B and T lymphocyte activity, for diagnosing and treating
 CC cancer, autoimmune disease, e.g. diabetes, pre-eclampsia, rheumatoid
 CC arthritis or multiple sclerosis, or infectious disease, or for preventing
 CC acute and/or chronic graft rejection.
 XX
 SQ Sequence 289 AA;

Query Match 100.0%; Score 1552; DB 8; Length 289;
 Best Local Similarity 100.0%; Pred. No. 8.1e-139;
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTLPAMLTGKLFWVFFLIPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFEECPV 60
 DB 1 MKTLPAMLTGKLFWVFFLIPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFEECPV 60
 QY 61 KYCANRPHVTWCKLNGTTCVKLEDQTSWKEEKNSFFILHPEPVLNDNGSYRCSANFQ 120
 DB 61 KYCANRPHVTWCKLNGTTCVKLEDQTSWKEEKNSFFILHPEPVLNDNGSYRCSANFQ 120
 QY 121 SNLIESHSTLYVTDVKASERPSKDEMASRPWLLYSLLPLGGLPLLIITTCFLCCLRR 180
 DB 121 SNLIESHSTLYVTDVKASERPSKDEMASRPWLLYSLLPLGGLPLLIITTCFLCCLRR 180
 QY 181 HQGQNELSDTAGREINLYDAHLKSEOTEASTRONSQVLLSETGIYDNDPDLCFRMOEGS 240
 DB 181 HQGQNELSDTAGREINLYDAHLKSEOTEASTRONSQVLLSETGIYDNDPDLCFRMOEGS 240
 QY 241 EYVSNPCLNEENPGIYVINSLSHNSVIGLSRLARNVKEAPTEYASICVRS 289
 DB 241 EYVSNPCLNEENPGIYVINSLSHNSVIGLSRLARNVKEAPTEYASICVRS 289

RESULT 2
 ADO43716
 ID ADO43716 standard; protein; 289 AA.
 XX
 AC ADO43716;
 XX
 XX 29-JUL-2004 (first entry)
 XX
 XX Amino acid sequence of PRO87299.
 DE human; PRO87299; gene therapy; tumour; immune related disease.
 KW Homo sapiens.
 XX
 XX Key Location/Qualifiers

FT Modified-site 31. .39 /note="tyrosine kinase phosphorylation site"
 FT Modified-site 41. .44 /note="CAMP- and CGMP-dependent protein kinase
 FT phosphorylation site"
 FT Domain 51. .117 /note = immunoglobulin domain
 FT Modified-site 75. .78 /note="N-glycosylation site"
 FT Modified-site 94. .97 /note="N-glycosylation site"
 FT Modified-site 110. .113 /note="N-glycosylation site"
 FT Modified-site 111. .116 /note="N-glycosylation site"
 FT Domain 153. .173 /note="N-myristoylation site"
 FT Modified-site 224. .229 /note = transmembrane domain
 FT Modified-site 254. .259 /note="N-myristoylation site"
 FT Domain 255. .260 /note = ITIM domain
 FT Modified-site 261. .264 /note="N-glycosylation site"
 FT Domain 280. .285 /note = ITISM domain
 PN WO2004039394-A1.
 XX 13-MAY-2004.
 XX
 PF 19-FEB-2003; 2003WO-US005335.
 PR 25-OCT-2002; 2002US-0421236P.
 XX (GETH) GENENTECH INC.
 PA Clark H, Eaton DL, Gurney AL, Wranik B;
 PI WPI; 2004-376066/35.
 XX N-PSDB; ADO43715.
 DR
 XX
 XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 9; Fig 2; 98pp; English.
 XX
 CC The present sequence represents a human polypeptide designated PRO87299.
 CC The polynucleotide is useful in molecular biology, including uses as
 CC hybridization probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, and in gene therapy. The polynucleotide may also
 CC be used in preparing PRO polypeptides by recombinant techniques, and in
 CC generating either transgenic animals or knock-out animals which, in turn,
 CC are useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptide is used in preparing a medicament for
 CC treating a condition responsive to the polypeptide, such as tumours and
 CC immune related diseases.
 XX
 SQ Sequence 289 AA;

Query Match 100.0%; Score 1552; DB 8; Length 289;
 Best Local Similarity 100.0%; Pred. No. 8.1e-139;
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTLPAMLTGKLFWVFFLIPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFEECPV 60
 DB 1 MKTLPAMLTGKLFWVFFLIPYLDIWNTHGKSCDQVLYIKRQSEHSILAGDPFEECPV 60
 QY 61 KYCANRPHVTWCKLNGTTCVKLEDQTSWKEEKNSFFILHPEPVLNDNGSYRCSANFQ 120
 DB 61 KYCANRPHVTWCKLNGTTCVKLEDQTSWKEEKNSFFILHPEPVLNDNGSYRCSANFQ 120

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 16:54:06 ; Search time 34.5 Seconds
(without alignments)
692.559 Million cell updates/sec

Title: US-10-600-997-6
Perfect score: 1552
Sequence: 1 MXTLPAMLTGKLFVFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	745.5	48.0	212	2	US-09-369-247-88
2	745.5	48.0	212	2	US-10-062-548-88
3	516	33.2	102	2	US-09-369-247-107
4	516	33.2	102	2	US-10-062-548-107
5	440	28.4	78	2	US-09-513-999C-7032
6	119.5	7.7	343	1	US-08-348-792-10
7	119.5	7.7	343	1	US-08-462-738-10
8	119.5	7.7	343	2	US-09-199-955-10
9	119.5	7.7	343	2	US-08-880-875-10
10	118	7.6	1953	2	US-09-317-254-92
11	113	7.3	624	1	US-08-642-406A-22
12	113	7.3	624	2	US-09-199-534-22
13	113	7.3	624	2	US-09-199-534-22
14	113	7.3	624	2	US-09-491-322-22
15	113	7.3	773	2	US-08-434-000A-2
16	113	7.3	773	2	US-09-312-157-2
17	113	7.3	773	2	US-09-717-888-2
18	113	7.3	773	2	US-09-818-247-6
19	105.5	6.8	278	2	US-09-270-767-42034
20	100.5	6.5	119	2	US-09-858-664A-30
21	100.5	6.5	119	2	US-10-274-978-31
22	100.5	6.5	119	2	US-10-697-263-31
23	100.5	6.5	739	2	US-09-854-845-45
24	100.5	6.5	744	2	US-09-854-845-43
25	100.5	6.5	838	2	US-09-854-845-29
26	100.5	6.5	843	2	US-09-854-845-27
27	99.5	6.4	329	1	US-08-348-792-12

28	99.5	6.4	329	1	US-08-462-738-12	Sequence 12, Appl
29	99.5	6.4	329	2	US-09-199-955-12	Sequence 12, Appl
30	99.5	6.4	329	2	US-08-880-875-12	Sequence 12, Appl
31	96.5	6.2	766	2	US-09-854-845-49	Sequence 49, Appl
32	96.5	6.2	771	2	US-09-854-845-47	Sequence 47, Appl
33	96.5	6.2	865	2	US-09-854-845-33	Sequence 33, Appl
34	96.5	6.2	870	2	US-09-854-845-31	Sequence 31, Appl
35	96	6.2	771	1	US-08-742-753-2	Sequence 2, Appl
36	92.5	6.0	1209	2	US-09-130-158A-2	Sequence 2, Appl
37	91.5	5.9	570	2	US-08-991-944-4	Sequence 4, Appl
38	91.5	5.9	570	2	US-09-173-151A-21	Sequence 21, Appl
39	91.5	5.9	622	2	US-09-499-846-2	Sequence 2, Appl
40	91.5	5.9	731	1	US-08-070-165F-10	Sequence 10, Appl
41	91.5	5.9	731	1	US-08-885-418-10	Sequence 10, Appl
42	90.5	5.8	816	1	US-07-640-029-1	Sequence 1, Appl
43	89.5	5.8	631	2	US-09-543-681A-7023	Sequence 7023, Ap
44	89.5	5.8	4391	2	US-10-006-011A-2	Sequence 2, Appl
45	89	5.7	820	1	US-08-166-717D-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-369-247-88
; Sequence 88, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 88
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-369-247-88

Query Match 48.0%; Score 745.5; DB 2; Length 212;
Best Local Similarity 95.1%; Pred. No. 4.6e-70;
Matches 137; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
QY 1 MXTLPAMLTGKLFVFFLIPLYLDIWNHKGSCDVQLYIKQSEHSILAGDPFELECPV 60
Db 1 MXTLPAMLTGKLFVFFLIPLYLDIWNHKGSCDVQLYIKQSEHSILAGDPFELECPV 60
QY 61 KYCANRPHVYTWCKLNGTTCVKLEDRQTSWKBEKNISFFILHPEPVLNDNGSYRCSANFQ 120
Db 61 KYCANRPHVYTWCKLNGTTCVKLEDRQTSWKBEKNISFFILHPEPVLNDNGSYRCSANFQ 120
QY 121 SNLIESHTLYVTVKASERPS 144
Db 121 SNLIESHTLYVTG-BFSTPRPS 143

RESULT 2
US-10-062-548-88
; Sequence 88, Application US/10062548
; Patent No. 6924356
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/10/062,548
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/369,247
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/074,118
; PRIOR FILING DATE: 1998-02-09
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; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,137
; PRIOR FILING DATE: 1998-02-09
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; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,141
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; GENERAL INFORMATION:
US-10-062-548-88

Query Match      48.0%; Score 745.5; DB 2; Length 212;
Best Local Similarity 95.1%; Pred. No. 4.6e-70;
Matches 137; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKTLPAMLTGKLFWVFFLIPLYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFEECPV 60
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Db 1 MKTLPAMLTGKLFWVFFLIPLYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFEECPV 60
   |||||

QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNI 120
   |||||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNI 120
   |||||

QY 121 SNLIESHSTLYVTGVKVSASERPS 144
   |||||
Db 121 SNLIESHSTLYVTG-EFSTPRPS 143
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RESULT 3
US-09-369-247-107
; Sequence 107, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (102)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-548-107

Query Match      33.2%; Score 516; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. No. 2e-46;
Matches 91; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNI 97
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Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNI 97
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RESULT 4
US-10-062-548-107
; Sequence 107, Application US/10062548
; Patent No. 6924356
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/10/062,548
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/369,247
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/074,118
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,157
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,137
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,341
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,141
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (102)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-548-107

Query Match      33.2%; Score 516; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. No. 2e-46;
Matches 91; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MKTLPAMLTGKLFWVFFLIPLYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFEECPV 60
   |||||

QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNI 97
   |||||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEEKNI 97
   |||||

RESULT 5
US-09-513-999C-7032
; Sequence 7032, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:56:11 ; Search time 10 Seconds
(without alignments)
379.241 Million cell updates/sec

Title: US-10-600-997-6

Perfect score: 1552

Sequence: 1 MKTLPAMLTGKLFVFFLI.....RLARNVKAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 1312538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1539	99.2	295	6	US-10-987-663-10
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4	90.5	5.8	822	7	US-11-183-567A-2
5	89.5	5.8	3588	6	US-10-995-561-672
6	89.5	5.8	4346	6	US-10-995-561-671
7	89.5	5.8	4347	6	US-10-995-561-670
8	89.5	5.8	4390	7	US-11-169-041-169
9	89.5	5.8	4419	6	US-10-821-234-1155
10	89	5.7	244	7	US-11-156-084-218
11	87	5.6	534	6	US-10-821-234-1341
12	86.5	5.6	976	7	US-11-148-770-31
13	86.5	5.6	1150	7	US-11-139-435-1
14	86.5	5.6	1338	6	US-11-109-156-23
15	85.5	5.5	1338	6	US-10-821-234-1622
16	85.5	5.5	2828	7	US-11-080-991-54
17	85.5	5.5	2828	7	US-11-186-284-49
18	85	5.5	309	6	US-10-453-372-778
19	83.5	5.4	305	6	US-11-000-463-391
20	83.5	5.4	398	6	US-10-821-234-1593
21	83.5	5.4	915	7	US-11-144-987-16
22	83.5	5.4	915	7	US-11-144-987-22
23	83.5	5.4	917	7	US-11-144-987-18
24	83.5	5.4	917	7	US-11-144-987-20
25	83.5	5.4	917	7	US-11-144-987-24

26	83.5	5.4	917	7	US-11-144-987-26	Sequence 26, Appl
27	83	5.3	399	7	US-11-159-919-4	Sequence 4, Appli
28	82.5	5.3	305	7	US-11-000-463-863	Sequence 863, App
29	82.5	5.3	4495	6	US-10-453-372-1002	Sequence 1002, Ap
30	82.5	5.3	5636	7	US-11-065-695-20	Sequence 20, Appl
31	82	5.3	977	7	US-11-093-274-39	Sequence 39, Appl
32	81	5.2	235	6	US-10-453-372-784	Sequence 784, App
33	81	5.2	284	6	US-10-453-372-790	Sequence 790, App
34	81	5.2	290	6	US-10-453-372-776	Sequence 776, App
35	81	5.2	302	6	US-10-453-372-780	Sequence 780, App
36	81	5.2	302	6	US-10-453-372-782	Sequence 782, App
37	81	5.2	302	6	US-10-453-372-788	Sequence 788, App
38	81	5.2	458	6	US-10-453-372-786	Sequence 786, App
39	81	5.2	464	6	US-10-453-372-772	Sequence 772, App
40	81	5.2	464	6	US-10-453-372-774	Sequence 774, App
41	81	5.2	473	6	US-10-453-372-770	Sequence 770, App
42	81	5.2	758	7	US-11-043-693-1	Sequence 1, Appli
43	80	5.2	136	7	US-11-156-084-324	Sequence 324, App
44	80	5.2	900	7	US-11-144-987-4	Sequence 4, Appli
45	80	5.2	902	7	US-11-144-987-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-987-663-2
; Sequence 2, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WEANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-2

Query Match 100.0%; Score 1552; DB 6; Length 289;
Best Local Similarity 100.0%; Pred. No. 3e-144;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKTLPAMLTGKLFVFFLI	1	MKTLPAMLTGKLFVFFLI	1	100.0%	1552	289	6	US-10-987-663-2	Sequence 26, Appl
DB	1	MKTLPAMLTGKLFVFFLI	1	MKTLPAMLTGKLFVFFLI	1	100.0%	1539	295	6	US-10-987-663-10	Sequence 4, Appli
QY	61	KYCANRPHVTWCKLNGTTCKVLEDRQTSWKEKNISFFLHPPEVLPNDNGSVRCSEANFQ	61	KYCANRPHVTWCKLNGTTCKVLEDRQTSWKEKNISFFLHPPEVLPNDNGSVRCSEANFQ	61	99.2%	1256	80.9	241	6	US-10-987-663-8
DB	61	KYCANRPHVTWCKLNGTTCKVLEDRQTSWKEKNISFFLHPPEVLPNDNGSVRCSEANFQ	61	KYCANRPHVTWCKLNGTTCKVLEDRQTSWKEKNISFFLHPPEVLPNDNGSVRCSEANFQ	61	80.5%	90.5	5.8	822	7	US-11-183-567A-2
QY	121	SNLIESHSITLYVTVDKASERPSKDEASRPWLLYSLLPLGLPLLIITTCFLCFLCLR	121	SNLIESHSITLYVTVDKASERPSKDEASRPWLLYSLLPLGLPLLIITTCFLCFLCLR	121	89.5%	89.5	5.8	3588	6	US-10-995-561-672
DB	121	SNLIESHSITLYVTVDKASERPSKDEASRPWLLYSLLPLGLPLLIITTCFLCFLCLR	121	SNLIESHSITLYVTVDKASERPSKDEASRPWLLYSLLPLGLPLLIITTCFLCFLCLR	121	89.5%	89.5	5.8	4346	6	US-10-995-561-671
QY	181	HQKQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSETGYDNDPDLCFRMEQGS	181	HQKQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSETGYDNDPDLCFRMEQGS	181	89.5%	89.5	5.8	4347	6	US-10-995-561-670
DB	181	HQKQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSETGYDNDPDLCFRMEQGS	181	HQKQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSETGYDNDPDLCFRMEQGS	181	89.5%	89.5	5.8	4390	7	US-11-169-041-169

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QY 241 EYVSNPCLEENKPGIVYASLNHSGVIGLSRLARNVKEAPTEYASICVRS 289
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Db 241 EYVSNPCLEENKPGIVYASLNHSGVIGLSRLARNVKEAPTEYASICVRS 289

RESULT 2
US-10-987-663-10
; Sequence 10, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-10

Query Match 99.2%; Score 1539; DB 6; Length 295;
Best Local Similarity 98.0%; Pred. No. 5.7e-143;
Matches 289; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MKTLPAMLTGKLFWVFFLIPYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFELECPV 60
|||||
Db 1 MKTLPAMLTGKLFWVFFLIPYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFELECPV 60

QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPVLNDNGSYRCSANFQ 120
|||||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPVLNDNGSYRCSANFQ 120

QY 121 SNLIESHSTTLVYVTVKASERPSKDEMASRPWLLYSLLPLGGLPLLITTCFCL 174
|||||
Db 121 SNLIESHSTTLVYVTVKASERPSKDEMASRPWLLYSLLPLGGLPLLITTCFCL 180

QY 175 FCCLRRHQKQNELSDTAGREINLVDAHLKSEQTEASTRQNSQVLLSETGIYNDPDLCF 234
|||||
Db 181 FCCLRRHQKQNELSDTAGREINLVDAHLKSEQTEASTRQNSQVLLSETGIYNDPDLCF 240

QY 235 RMOEGSEVYVSNPCLEENKPGIVYASLNHSGVIGLSRLARNVKEAPTEYASICVRS 289
|||||
Db 241 RMOEGSEVYVSNPCLEENKPGIVYASLNHSGVIGLSRLARNVKEAPTEYASICVRS 295

RESULT 3
US-10-987-663-8
; Sequence 8, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; FILE REFERENCE: P1996R1P1-US
```

```
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 8
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-8

Query Match 80.9%; Score 1256; DB 6; Length 241;
Best Local Similarity 83.4%; Pred. No. 1.9e-115;
Matches 241; Conservative 0; Mismatches 0; Indels 48; Gaps 1;

QY 1 MKTLPAMLTGKLFWVFFLIPYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFELECPV 60
|||||
Db 1 MKTLPAMLTGKLFWVFFLIPYLDIWNHKGSCDVQLYIKRQSEHSILAGDPFELECPV 60

QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPVLNDNGSYRCSANFQ 120
|||||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPVLNDNGSYRCSANFQ 120

QY 121 SNLIESHSTTLVYVTVKASERPSKDEMASRPWLLYSLLPLGGLPLLITTCFCLFCCLLR 180
|||||
Db 121 SNLIESHSTTLVYVTVKASERPSKDEMASRPWLLYSLLPLGGLPLLITTCFCLFCCLLR 134

QY 181 HOGKQNELSDTAGREINLVDAHLKSEQTEASTRQNSQVLLSETGIYNDPDLCFRMOEGS 240
|||||
Db 135 --GKQNELSDTAGREINLVDAHLKSEQTEASTRQNSQVLLSETGIYNDPDLCFRMOEGS 192

QY 241 EYVSNPCLEENKPGIVYASLNHSGVIGLSRLARNVKEAPTEYASICVRS 289
|||||
Db 193 EYVSNPCLEENKPGIVYASLNHSGVIGLSRLARNVKEAPTEYASICVRS 241

RESULT 4
US-11-183-567A-2
; Sequence 2, Application US/11183567A
; Publication No. US20060019296A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Ming-Ming
; APPLICANT: Goldfarb, Mitchell
; TITLE OF INVENTION: Methods of Identifying Modulators of the
; FILE REFERENCE: 2459-1-002NCON
; CURRENT APPLICATION NUMBER: US/11/183,567A
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: 09/757,415
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,867
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-567A-2

Query Match 5.8%; Score 90.5; DB 7; Length 822;
Best Local Similarity 22.0%; Pred. No. 0.67;
Matches 69; Conservative 43; Mismatches 118; Indels 83; Gaps 17;

QY 27 NIHGKSCDVQLYIKRQSEH-----SILAGDPFELECPVKTCANRPHVTWCK- 73
|||||
Db 234 NEYGSINHTYQLDVVVERSPHRPILOAGLPANETVAGSNVNEFWCKV-YSDPQPHIQWLKH 292
|||||
QY 74 --LNGCT-----TCVKLEDRQTSWKEKNISFFILHPEPVLNDNGSYRCSANFQS 121
|||||
Db 293 IEVNGSKIGPDNLPYVQILKTAGVNTTDKEME-----VLHLRNVSFEDAGEYTCLAGNSI 347
```


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OM protein - protein search, using sw model

Run on: February 8, 2006, 16:48:30 ; Search time 26.5 Seconds
(without alignments)
1049.307 Million cell updates/sec

Title: US-10-600-997-6
Perfect score: 1552
Sequence: 1 MKTLPAMLTGKLFVWFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	121	7.8	6642	2 T29757	protein UNC-89 - C
2	113.5	7.3	841	2 JCS894	killer cell inhibi
3	113	7.3	773	1 QRRRG	secretory componen
4	112	7.2	335	2 A53434	cell surface glyco
5	107.5	6.9	1036	2 S22383	axonin 1 precursor
6	102	6.6	1852	2 A37860	calcium channel pr
7	101.5	6.5	812	1 A36477	fibroblast growth
8	100.5	6.5	5175	2 T20992	hypothetical prote
9	100.5	6.5	5198	2 T43290	hemocentin precurs
10	99.5	6.4	1336	2 I60598	Fit-1 tyrosine kin
11	98	6.3	7962	2 I38346	elastic titin - hu
12	97.5	6.3	806	2 A35963	protein-tyrosine k
13	97.5	6.3	1158	2 S33901	reverse transcript
14	96	6.2	3707	2 S18252	heparan sulfate pr
15	95.5	6.2	814	1 A39752	fibroblast growth
16	95	6.1	978	1 A49814	protein-tyrosine k
17	95	6.1	1277	2 T30532	neural cell adhesi
18	93.5	6.0	210	2 S25657	T-cell surface gly
19	93.5	6.0	296	2 B53434	cell surface glyco
20	92.5	6.0	303	2 A40807	membrane glycoprot
21	92.5	6.0	480	2 A56182	hypothetical prote
22	92.5	6.0	1177	2 T16594	fibroblast growth
23	92.5	6.0	1507	2 T42631	breast cancer tumo
24	91.5	5.9	210	2 E46482	T-cell surface gly
25	91.5	5.9	221	2 C46482	T cell surface gly
26	91.5	5.9	246	2 T01073	T cell surface gly
27	91.5	5.9	570	2 A57535	intrileukin 1 recep
28	91.5	5.9	6805	2 S20901	titin - rabbit (fir
29	91	5.9	632	2 T18692	hypothetical prote

30	91	5.9	769	2 S36657	SWI6 protein - yea
31	90.5	5.8	192	2 I39464	CD8 antigen - huma
32	90.5	5.8	729	2 A56795	fibroblast growth
33	90.5	5.8	733	2 I49293	fibroblast growth
34	90.5	5.8	822	1 TVMSFG	fibroblast growth
35	90.5	5.8	822	2 I45289	fibroblast growth
36	90.5	5.8	832	2 JH0393	fibroblast growth
37	90	5.8	761	2 B69797	transcription regu
38	90	5.8	1209	2 T42718	probable neural ce
39	89.5	5.8	750	2 S41051	fibroblast growth
40	89.5	5.8	1694	2 S50065	sialoadhesin - mou
41	89.5	5.8	4391	2 A38096	perlecan precursor
42	89	5.7	244	2 AD1834	isopentenyl transf
43	88.5	5.7	246	2 D46482	T-cell surface gly
44	88.5	5.7	797	2 S38579	fibroblast growth
45	88.5	5.7	813	1 A49123	fibroblast growth

ALIGNMENTS

RESULT 1

T29757 protein UNC-89 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C:Accession: T29757
R:Du, Z.; Le, T.T.; Wilson, R.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid C09D1.
A:Reference number: Z20679
A:Accession: T29757
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6642 <DUZ>
A:Cross-references: UNIPARC:UPI000017CF3C; EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN0001
A:Experimental source: strain Bristol N2; clone C09D1
C:Genetics:
A:Gene: CBSP:unc-89
A:Map position: 1
A:Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1;
/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

Query Match	7.8%;	Score 121;	DB 2;	Length 6642;
Best Local Similarity	23.4%;	Pred. No. 0.35;		
Matches	48;	Conservative 24;	Mismatches 69;	Indels 64; Gaps 7;
QY	27	NIHGK-----	ESCDVOL-----	-----YIKROSEHSILAGDPPELECPVKYCAN 65
Db	5574	NAHGKAKTQATAHVQWALGKTEKPKMDEGKPKFILELSDMSVSLGNVIDLECKVTGLPN 5633		
QY	66	RPHVTWCKLNGTTCVKLEDRQTSWKEKNISFPILHPEPVLNDNGSVYCSANFQSNLIE 125		
Db	5634	-PSVKMSKDGGL-----	IBDSRFWNSKSGVYQLRKIVATVHDEGTYTCVATNENGSA 5689	
QY	126	SHS-----	TLTYTDVKSASERPSKDE-----	-----MASRPW----- 153
Db	5690	TKSFVRMDGLSGGVVTASQPPRFILKMGDVATTEGQPLKLECKVDASLPENWVYKOGA 5749		
QY	154	-----	LLYSLLPLGGLPLITTC 171	
Db	5750	IVTPSDRIQISLSPDGVATLLIPSC 5774		

RESULT 2

JCS894 killer cell inhibitory receptor p91A precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 09-Jul-2004
C:Accession: JCS894
R:Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohy
J. Biochem. 123, 358-368, 1998
A>Title: Genomic structures and chromosomal location of p91, a novel murine regulatory

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OM protein - protein search, using sw model

Run on: February 8, 2006, 16:43:35 ; Search time 164 Seconds
(without alignments)
1243.279 Million cell updates/sec

Title: US-10-600-997-6
Perfect score: 1552
Sequence: 1 MKTLPAMLGKGLFWFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.4

1: uniprot_sprot.4

2: uniprot_trembl.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1552	100.0	289	1	BTLA HUMAN
2	733.5	47.3	306	1	Q7tea3 mus musculus
3	694.5	44.7	308	1	Q6pm1 rattus norv
4	121	7.8	592	2	Q5w615 caenorhabdi
5	121	7.8	632	1	Q01761 caenorhabdi
6	121	7.8	712	2	Q5w616 caenorhabdi
7	121	7.8	744	2	Q5w617 caenorhabdi
8	121	7.8	808	2	Q72120 caenorhabdi
9	119.5	7.7	266	2	Q9CUC8 MOUSE
10	119.5	7.7	343	1	SLAF1 MOUSE
11	119.5	7.7	343	2	Q544K1 MOUSE
12	118	7.6	1914	1	MYLK HUMAN
13	117	7.5	1914	2	Q5MY99 HUMAN
14	117	7.5	1914	2	Q724J0 HUMAN
15	115	7.4	841	2	Q97484 MOUSE
16	113.5	7.3	841	2	Q8R221 MOUSE
17	113	7.3	773	1	PICR RABIT
18	112	7.2	335	1	LIRN4 MOUSE
19	107.5	6.9	1036	1	CNTN2 CHICK
20	107	6.9	1272	2	Q5G1T3 BRARE
21	105.5	6.8	265	2	Q81P93 DROME
22	105.5	6.8	298	2	Q96114 DROME
23	105	6.8	428	2	Q6F3J3 MOUSE
24	105	6.8	1272	2	Q4JDD5 BRARE
25	104.5	6.7	1845	2	Q5MYA0 HUMAN
26	103.5	6.7	1029	2	Q6ZJE3 ORYSA
27	103.5	6.7	1271	2	Q6U714 BRARE
28	103	6.6	376	2	Q67EV3 RAT
29	103	6.6	841	2	Q54999 MOUSE
30	103	6.6	1026	1	CNTN4 RAT
31	102	6.6	532	2	Q4Q815 LEISHMA

32	102	6.6	1852	1	CACIS_CYPCA
33	101.5	6.5	810	2	Q9PS96_XENLA
34	101.5	6.5	812	1	QGFRI_XENLA
35	100.5	6.5	335	2	Q90745_CHICK
36	100.5	6.5	838	1	SEM4G_HUMAN
37	100.5	6.5	838	2	Q58BY1_HUMAN
38	100.5	6.5	5175	2	Q810L3_CAEEL
39	100.5	6.5	5198	2	Q76518_CAEEL
40	99.5	6.4	326	2	Q8CAU4_MOUSE
41	99.5	6.4	904	2	Q4HXS1_GIBZE
42	99.5	6.4	1336	1	VGPR1_RAT
43	99	6.4	3950	2	Q7YRF5_CANFA
44	99	6.4	10495	2	Q4RE92_TETNG
45	98	6.3	837	1	SEM4G_MOUSE

P22316	cyprinus ca
Q9PS96	xenopus lae
P22182	xenopus lae
Q90746	gallus gall
Q9ntn9	homo sapien
Q58ey1	homo sapien
Q81013	caenorhabdi
Q76518	caenorhabdi
Q8CAU4	mus musculu
Q4HXS1	gibberella
P53767	rattus norv
Q7YRF5	canis famil
Q4RE92	tetradon n
Q9WUH7	mus musculu

ALIGNMENTS

RESULT 1
BTLA_HUMAN
ID BTLA_HUMAN STANDARD; PRT; 289 AA.
AC Q7Z6A9; Q6ZNH9;
DT 13-SBP-2005 (Rel. 48, Created)
DT 13-SBP-2005 (Rel. 48, Last sequence update)
DT 13-SBP-2005 (Rel. 48, Last annotation update)
DE B and T lymphocyte attenuator precursor (B and T lymphocyte-associated protein).
DE protein).
GN Name=BTLA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], MUTAGENESIS OF TYR-226; TYR-257 AND TYR-282, N-GLYCOSYLATION, FUNCTION, AND INTERACTIONS WITH PTPN6 AND PTPN11.
RX PubMed=12796776; DOI=10.1038/nr1944;
RA Watanabe N., Gavrieli M., Sedy J.R., Yang J., Fallarino F., Loftin S.K., Hurchla M.A., Zimmerman N., Sim J., Zang X., Murphy T.L., Russell J.H., Allison J.P., Murphy K.M.;
RA "BTLA is a lymphocyte inhibitory receptor with similarities to CTLA-4 and PD-1.";
RT Nat. Immunol. 4:670-679(2003).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 4-289.
TISSUE=Trachea;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togaiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara Y., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

FT	MUTAGEN	282	282	phosphorylation; when associated with F-226 and/or F-282.
FT				Y->P: No change of phosphorylation
FT				implicated in interaction with PTPN6 and
FT				PTPN11. Severe reduction of
FT				phosphorylation; when associated with F-226 and/or F-257.
FT	CONFLICT	105	105	V -> M (in Ref. 1).
FT	CONFLICT	138	138	S -> G (in Ref. 1).
FT	CONFLICT	148	148	M -> V (in Ref. 1).
FT	CONFLICT	171	171	C -> W (in Ref. 1).
FT	CONFLICT	219	219	L -> P (in Ref. 2).
FT	CONFLICT	223	223	T -> A (in Ref. 1).
FT	CONFLICT	243	243	Y -> C (in Ref. 1).
SEQ	SEQUENCE	289 AA;	32781 MW;	98D1FE325D882642 CRC64;
Query Match 100.0%; Score 1552; DB 1; Length 289;				
Best Local Similarity 100.0%; Pred. No. 1.9e-123;				
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	MKTLPAMLGKGLFWFFFLPYLDIWNHKGESCDVOLYIKRQSEHILAGDPPELECPV	60	
Db	1	MKTLPAMLGKGLFWFFFLPYLDIWNHKGESCDVOLYIKRQSEHILAGDPPELECPV	60	
Qy	61	KYCANRPHVTWCKLNGTTTCVKLEDROTQSWKEKNISFFILHFEVPLENDNGSYRCSANFQ	120	
Db	61	KYCANRPHVTWCKLNGTTTCVKLEDROTQSWKEKNISFFILHFEVPLENDNGSYRCSANFQ	120	
Qy	121	SNLIESHTTLYVTDVKASERPSKDEMARPMLLYSLLPLGGGLPLLITTCFCLFCCLLRR	180	
Db	121	SNLIESHTTLYVTDVKASERPSKDEMARPMLLYSLLPLGGGLPLLITTCFCLFCCLLRR	180	
Qy	181	HQKQNELSDTAGREINLVDHLKSEQTEASTQNQSVLLSETGIYDNDPDLCFRMOEGS	240	
Db	181	HQKQNELSDTAGREINLVDHLKSEQTEASTQNQSVLLSETGIYDNDPDLCFRMOEGS	240	
Qy	241	EVYSNPNCLEENKPGIVVYASLNHNSVIGUNSLARNVKEAPTEYASICVRS	289	
Db	241	EVYSNPNCLEENKPGIVVYASLNHNSVIGUNSLARNVKEAPTEYASICVRS	289	
RESULT 2				
BTLA_MOUSE	BTLA_MOUSE	STANDARD;	PTI;	306 AA.
AC	QTS3;			
DT	13-SEP-2005 (Rel. 48, Created)			
DT	13-SEP-2005 (Rel. 48, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	B and T lymphocyte attenuator precursor (B and T lymphocyte-associated protein).			
DE	NCBI_TaxID=10090;			
GN	Name=Btla;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [mRNA] (ISOFORMS 1 AND 2), MUTAGENESIS OF TYR-245;			
RP	TYR-274 AND TYR-299, N-GLYCOSYLATION, TISSUE SPECIFICITY, INTERACTIONS			
RP	WITH PTPN6 AND PTPN11, AND VARIANTS GLU-41; 45-ASN--LYS-47; HIS-52;			
RP	TRP-55; GLU-63; TRP-85; GLY-91 AND ARG-102.			
RC	STRAIN=129/SvEv;			
RC	PubMed=12796776; DOI=10.1038/ni944;			
RA	Watanabe N., Gavriel M., Sedy J.R., Yang J., Pallarino F.,			
RA	Loftin S.K., Hurchia M.A., Zimmerman N., Sim J., Zang X., Murphy T.L.,			
RA	Russell J.H., Allison J.P., Murphy K.M.;			
RT	"BTla is a lymphocyte inhibitory receptor with similarities to CTLA-4			
RT	and PD-1";			
RL	Nat. Immunol. 4:670-679(2003).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3), AND VARIANT			
RP	THR-143.			
RC	STRAIN=C57BL/6J; TISSUE=Thymus;			

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 05:19:46 ; Search time 649 Seconds
(without alignments)
8934.180 Million cell updates/sec

Title: US-10-600-997-7
Perfect score: 870
Sequence: 1 atgaagacattgcctgccat.....ccatattgtgaggagtaa 870

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

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- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	870	12	ADH34663 Human BTL
2	870	100.0	870	14	ADX01460 Human tol
3	857.2	98.5	870	13	ADU51091 Human spl
4	857.2	98.5	990	13	ADU51153 Human spl
5	854	98.2	916	12	ADH74501 Human mcd
6	854	98.2	1066	12	ADU43715 Human mcd
7	854	98.2	1066	14	AEA23329 Human ant
8	846	97.2	3002	12	ADH74499 Human mcd
9	833	95.7	849	12	ADH74497 Human mcd
10	764.2	87.8	777	13	ADU51090 Human spl
11	704.2	80.9	717	13	ADU51089 Human spl
12	564	64.8	1014	6	AB876365 DNA encod
13	527.6	60.6	534	13	ADU51085 Human SPE
14	520.2	59.8	726	2	AAV88865 Human SPE
15	466.2	53.6	471	13	ADU51083 Human SPE
16	437.6	50.3	444	13	ADU51084 Human SPE
17	425	48.9	769	14	ADY19217 DNA encod
18	402.8	46.3	1903	2	AZ00830 Human sec
19	402.8	46.3	1903	8	ADA40232 Human sec

20	402.8	46.3	1903	10	ADA56392	Ada56392 Gene enco
21	388	44.6	396	13	ADU51088	Adus1088 Human SPE
22	378	43.4	1940	2	AZ00850	Az00850 Human sec
23	378	43.4	1940	8	ADA40551	Ada40551 Human sec
24	378	43.4	1940	10	ADA56697	Ada56697 Gene enco
25	376.2	43.2	381	13	ADU51082	Adus1082 Human SPE
26	326.6	37.5	333	13	ADU51087	Adus1087 Human spl
27	276.6	31.8	422	10	ADP81166	Adf81166 Leukaemia
28	276.6	31.8	465	10	ADP82536	Adf82536 Leukaemia
29	275.6	31.7	921	12	ADH34665	Adh34665 Mouse BTL
30	270.6	31.1	3229	14	ADX01473	Adx01473 Human tol
31	267.6	30.8	921	13	ADU51133	Adus1133 Murine sp
32	267.6	30.8	1250	13	ADU51154	Adus1154 Murine sp
33	267.6	30.8	1276	13	ADU51158	Adus1158 Murine sp
34	264.6	30.4	957	13	ADU51155	Adus1155 Murine sp
35	264.6	30.4	1722	13	ADU51156	Adus1156 Murine sp
36	254.2	29.2	831	13	ADU51132	Adus1132 Murine sp
37	236.8	27.2	750	13	ADU51131	Adus1131 Murine SP
38	233	26.8	319	3	AAC02957	Aac02957 Human sec
39	199.4	22.9	201	13	ADU51073	Adus1073 Human spl
40	198.4	22.8	201	13	ADU51086	Adus1086 Human SPE
41	157.2	18.1	537	13	ADU51138	Adus1138 Murine SP
42	157.2	18.1	537	13	ADU51162	Adus1162 Murine sp
43	156.4	18.0	378	13	ADU51130	Adus1130 Murine SP
44	149.2	17.1	540	13	ADU51125	Adus1125 Murine SP
45	149.2	17.1	612	13	ADU51127	Adus1127 Murine SP

ALIGNMENTS

RESULT 1
ADH34663
ID ADH34663 standard; cDNA; 870 BP.
XX
AC ADH34663;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human BTLA coding sequence.
XX
KW B7x; ligand; B and T lymphocyte attenuator; BTLA; tumour; inhibition;
tumour-specific; immunological tolerance; cancer; autoimmune disease;
diabetes; pre-eclampsia; rheumatoid arthritis; multiple sclerosis;
infection; graft rejection; cell cycle progression; differentiation;
survival; cytokine production; cytolytic activation;
antigen presentation; antibody production; ss; gene.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1..870
FT /*tag= a
FT /product= "Human BTLA"
FT
FT WO2004000221-A2.
XX
PD 31-DEC-2003.
XX
PF 20-JUN-2003; 2003WO-US019614.
XX
PP Aea23329 Tumour ant
PR Aea23329 Human mcd
PR Adh74499 Human mcd
PR Adh74497 Human mcd
PR Adus1090 Human spl
PR Adus1089 Human SPE
PA Ab876365 DNA encod
XX Aav88865 Human SPE
PI Aav88865 EST clone
XX Adus1083 Human SPE
XX Adus1084 Human SPE
DR Ady19217 DNA encod
XX Az00830 Human sec
PT Ada40232 Human sec

New recombinant B and T lymphocyte attenuator nucleic acid and protein,

useful for modulating B and T lymphocyte activity, or for diagnosing and treating cancer, autoimmune disease or infectious disease.

E

Claim 64: Fig 28: 121pp: English.

This sequence encodes a human B and T lymphocyte attenuator (BTLA). BTLA acts as a negative regulator of both B and T lymphocyte activity, where signaling mediated by BTLA results in the inhibition of BTLA-positive lymphocyte activity. In BTLA-positive T cells BTLA signalling can inhibit TCR-induced T cell responses, such as cell cycle progression, differentiation, survival, cytokine production and cytolytic activation. In BTLA-positive B cells BTLA signalling can inhibit B cell antigen receptor-induced B cell responses, such as cell cycle progression, differentiation, survival, antigen presentation and antibody production. B7x is a ligand for the recombinant BTLA of the invention. B7x is able to negatively regulate B and T lymphocyte activity through its interaction with BTLA, which inhibits both B and T cell responses. Therefore B7x positive tumour tissue inhibits the activity of tumour-specific T cells. B7x is also expressed on non-tumour non-lymphoid tissue, showing that the B7x/BTLA interaction is a mechanism for maintaining immunological tolerance. BTLA proteins and related nucleic acids are useful for modulating B and T lymphocyte activity, for diagnosing and treating cancer, autoimmune disease, e.g. diabetes, pre-eclampsia, rheumatoid arthritis or multiple sclerosis, or infectious disease, or for preventing acute and/or chronic graft rejection.

Sequence 870 BP; 272 A; 185 C; 185 G; 228 T; 0 U; 0 Other;

Query Match	100.0%;	Score 870;	DB 12;	Length 870;
Best Local Similarity	100.0%;	Pred. No. 5.5e-251;		
Matches 870; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAGACATTCGCTGCCATGCTTCGAACTCGGAATTTATTTTCGGTCTTCTCTCTTAATC	60	
DB	1	ATGAAGACATTCGCTGCCATGCTTCGAACTCGGAATTTATTTTCGGTCTTCTCTCTTAATC	60	
QY	61	CCATATCTCGACATCTGGAAACATCCATCGGAAAGAAATCATGTGATGTACAGCTTTATATA	120	
DB	61	CCATATCTCGACATCTGGAAACATCCATCGGAAAGAAATCATGTGATGTACAGCTTTATATA	120	
QY	121	AGAGACAATCTGACACATCCATCTTAGCAGGAGATCCCTTTGAACTAGAGATGCCCTGTG	180	
DB	121	AGAGACAATCTGACACATCCATCTTAGCAGGAGATCCCTTTGAACTAGAGATGCCCTGTG	180	
QY	181	AAATACTGTGCTAAACAGGCCCTCATGTGACTTTGGTGCAGCTCAATGGAAACAATGTGTA	240	
DB	181	AAATACTGTGCTAAACAGGCCCTCATGTGACTTTGGTGCAGCTCAATGGAAACAATGTGTA	240	
QY	241	AAACTTGAAGATAGACAAACAAGTTGGAAAGNAGAGAAACATTTCATTTTTCATCTTA	300	
DB	241	AAACTTGAAGATAGACAAACAAGTTGGAAAGNAGAGAAACATTTCATTTTTCATCTTA	300	
QY	301	CATTTTGAACCAATGCTTCTTAATGACAAATGGGTCAACCGCTGTTCTGCAAAATTTTCAG	360	
DB	301	CATTTTGAACCAATGCTTCTTAATGACAAATGGGTCAACCGCTGTTCTGCAAAATTTTCAG	360	
QY	361	TCTAAATCTCATTTGAAAGCCACTCAACAACTCTTTATGTGACAGATGTAAAAGGTGCCTCA	420	
DB	361	TCTAAATCTCATTTGAAAGCCACTCAACAACTCTTTATGTGACAGATGTAAAAGGTGCCTCA	420	
QY	421	GAACGACCTTCCAAAGGACGAAGTGCACAGACCCCTGGCTCCGTGATAGTTTACTTCCT	480	
DB	421	GAACGACCTTCCAAAGGACGAAGTGCACAGACCCCTGGCTCCGTGATAGTTTACTTCCT	480	
QY	481	TTGGGGGGATTCGCTTACTCATCTACTACCTTGTTCGCTGTTTCGCTGCCTGAGAAGG	540	
DB	481	TTGGGGGGATTCGCTTACTCATCTACTACCTTGTTCGCTGTTTCGCTGCCTGAGAAGG	540	
QY	541	CACCAAGGAAGCAAAATGAACTCTTGACACAGCAGGAGGGAATTAATCTGTTGAT	600	
DB	541	CACCAAGGAAGCAAAATGAACTCTCTGACACAGCAGGAGGGAATTAATCTGTTGAT	600	
QY	601	GCTCACCTTTAAGAGCGAGCAAAACAGAAAGCAACGACACAGGCAAAATTCCTCAAGTACTGCTA	660	

Db	601	GCTCACCTTAAAGAGCGAGCAACAGAAACAAGCACAGGCAAAATTC	CCAGTACTGCTA	660
Qy	661	TCAGAAGCTGGAAATTATGATAATGACCCCTGACCTTTGTTTC	CAGGATGCAGGAAGGGTCT	720
Db	661	TCAGAAGCTGGAAATTATGATAATGACCCCTGACCTTTGTTTC	CAGGATGCAGGAAGGGTCT	720
Qy	721	GAAGTTTGTTCTTAATCCATGCTCGAAGCAAAACAACAGGCAATG	TTTATGCTTCCCTCG	780
Db	721	GAAGTTTGTTCTTAATCCATGCTCGAAGCAAAACAACAGGCAATG	TTTATGCTTCCCTCG	780
Qy	781	AACCATTCGTCAATGGACTGAACCTCAAGACTGGCAAGAATGT	TAAGAAGACCAACCA	840
Db	781	AACCATTCGTCAATGGACTGAACCTCAAGACTGGCAAGAATGT	TAAGAAGACCAACCA	840
Qy	841	GAATATGCATCCATATGTGTGAGGAGTTAA	870	
Db	841	GAATATGCATCCATATGTGTGAGGAGTTAA	870	

RESULT 2
ADX01460

ADX01460
ID ADX01460 standard; DNA; 870 BP.

AC ADX01460:

DT 21-APR-2005 (first entry)

Human tolerance target molecule #33.

Screening; immune disorder; autoimmune disease; transplant rejection; diabetes mellitus; arthritis; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; systemic lupus erythematosus; Hashimoto disease; dermatitis; psoriasis; ulcerative colitis; scleroderma; female genital tract inflammation; Crohns disease; sarcoidosis; pulmonary fibrosis; immunosuppressive; antidiabetic; antiarthritic; antirheumatic; neuroprotective; muscular-gen.; antiinflammatory; dermatological; antithyroid; antipsoriatic; anticancer; gastrointestinal-gen.; respiratory-gen.; cytostatic; virucide; gene; ds

XX Homo sapiens.

XX PN WO2005010215-A2.

XX
PD 03-FEB-2005.XX
PF
19-JUL-2004: 2004WO-US023309.

PR 17-JUL-2003: 2003US-0488502P.

XX
PA (TOLE-) TOLERRX INC.XX
PI Rao P. Snyder J. Bagley A:XX
DR WPI: 2005-123168/13.

xx PT Identifying a tolerance modulatory compound, useful for reducing T
PT effector (Teff) cell function or increasing T regulatory (Treg) cell
PT function, by assaying for expression or activity of Treg marker and Teff
PT marker.

XX
PS Disclosure: SEO ID NO 33: 149pp: English:

The invention relates to a method of identifying a tolerance modulatory compound comprising assaying for expression or activity of at least one regulatory (Treg) marker and at least one T effector (Teff) marker, where a change in expression or activity of the Treg marker or the Teff marker and/or an inverse change in expression or activity of the Teff marker identifies the test compound as a tolerance modulatory compound. The method comprises contacting a cell with a stimulating agent and a test compound and assaying for expression or activity of at least one Treg marker and at least one Teff marker. The invention also relates to a method of identifying a tolerance promoting compound and a method of

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 05:36:22 ; Search time 909 Seconds
(without alignments)
7914.586 Million cell updates/sec

Title: US-10-600-997-7

Perfect score: 870
Sequence: 1 atgaagacattgcctgccat.....ccatattgtgaggagtaa 870

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:
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3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	DB ID	Description
1	870	100.0	870 7	US-10-600-997-7
2	870	100.0	870 9	US-10-895-225A-33
3	857.2	98.5	870 8	US-10-831-622-42
4	857.2	98.5	870 9	US-10-964-215-42
5	857.2	98.5	990 8	US-10-831-622-104
6	857.2	98.5	990 9	US-10-964-215-104
7	854	98.2	1066 7	US-10-371-341-1
8	854	98.2	1066 8	US-10-989-826-27
9	764.2	87.8	777 8	US-10-831-622-41
10	764.2	87.8	777 9	US-10-964-215-41
11	704.2	80.9	717 8	US-10-831-622-40
12	704.2	80.9	717 9	US-10-964-215-40
13	564	64.8	1014 7	US-10-471-449-22
14	527.6	60.6	534 8	US-10-831-622-36
15	527.6	60.6	534 9	US-10-964-215-36
16	520.2	59.8	726 5	US-10-040-739-1343
17	466.2	53.6	471 8	US-10-831-622-34
18	466.2	53.6	471 9	US-10-964-215-34
19	437.6	50.3	444 8	US-10-831-622-35
20	437.6	50.3	444 9	US-10-964-215-35
21	402.8	46.3	1903 5	US-10-062-548-39
22	402.8	46.3	1903 8	US-10-918-446-39
23	402.8	46.3	1903 10	US-11-002-755-39

ALIGNMENTS

RESULT 1

US-10-600-997-7

; Sequence 7, Application US/10600997

; Publication No. US20040175380A1

; GENERAL INFORMATION:

; APPLICANT: Allison, James

; APPLICANT: Murphy, Kenneth

; APPLICANT: Watanabe, Norihiko

; APPLICANT: Murphy, Theresa

; APPLICANT: Yang, Jianfei

; APPLICANT: Zang, Xingxing

; TITLE OF INVENTION: Compositions and Methods for Modulating Lymphocyte Activity

; FILE REFERENCE: A-71608/TAL/DHR

; CURRENT APPLICATION NUMBER: US/10/600,997

; CURRENT FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: US 60/390,653

; PRIOR FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: US 60/438,593

; PRIOR FILING DATE: 2003-01-06

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7

; LENGTH: 870

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-600-997-7

Query Match 100.0%; Score 870; DB 7; Length 870;

Best Local Similarity 100.0%; Pred. No. 3.7e-251;

Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGACATTCGCTGCCATCTTGGAACTGGGAATATTTGGGTCTTCTTAAATC 60

Db 1 ATGAGACATTCGCTGCCATCTTGGAACTGGGAATATTTGGGTCTTCTTAAATC 60

QY 61 CCATATCTGGACATCTGGACATCCATCTTAGCAGAGATCCCTTTGAACTAGAACTGCTTATATA 120

Db 61 CCATATCTGGACATCTGGACATCCATCTTAGCAGAGATCCCTTTGAACTAGAACTGCTTATATA 120

QY 121 AAGAGACATCTGAACTCCATCTTAGCAGAGATCCCTTTGAACTAGAACTGCTTATATA 180

Db 121 AAGAGACATCTGAACTCCATCTTAGCAGAGATCCCTTTGAACTAGAACTGCTTATATA 180

QY 181 AAATACTGTGCTAACAGGCTCATGTGCTTGGTCAAGCTCAATGGAACAAATGTGTA 240

Db 181 AAATACTGTGCTAACAGGCTCATGTGCTTGGTCAAGCTCAATGGAACAAATGTGTA 240

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 05:26:42 ; Search time 4815 Seconds
(without alignments)
10270.779 Million cell updates/sec

Title: US-10-600-997-7

Perfect score: 870

Sequence: 1 atgaagacattgcctgccat.....ccatatgtgtgaggagtgtaa 870

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 5881141 seqs, 2842172553 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	870	8	AY293286 Homo sapi
2	857.2	98.5	870	6	CQ947366 Sequence
3	857.2	98.5	990	6	CQ947428 Sequence
4	854	98.2	1066	6	CS105855 Sequence
5	846	97.2	3002	8	AK131204 Homo sapi
6	764.2	87.8	777	6	CQ947365 Sequence
7	704.2	80.9	717	6	CQ947364 Sequence
8	527.6	60.6	534	6	CQ947360 Sequence
9	520.2	59.8	726	6	BD060983 Secreted
10	466.2	53.6	471	6	CQ947358 Sequence
11	437.6	50.3	444	6	CQ947359 Sequence
12	425	48.9	769	6	CS035517 Sequence
13	425	48.9	769	6	CS044469 Sequence
14	402.8	46.3	1903	6	BD131124 45 human
15	402.8	46.3	1903	6	CS132603 Sequence
16	402.8	46.3	1903	6	AR339778 Sequence
17	388	44.6	396	6	CQ947363 Sequence
18	378	43.4	1940	6	BD131144 45 human

19	378	43.4	1940	6	CS132623	Sequence
20	378	43.4	1940	6	AR339797	Sequence
21	376.2	43.2	381	6	CQ947357	Sequence
22	326.6	37.5	333	6	CQ947362	Sequence
23	315.8	36.3	127852	8	AC092894	Homo sapi
24	315.8	36.3	143094	14	AC024131	Sequence
25	315.8	36.3	175135	14	AC079211	Sequence
26	285.2	32.8	2230	9	BC092588	Rattus no
27	276.6	31.8	422	6	AX779565	Sequence
28	276.6	31.8	465	6	AX780935	Sequence
29	275.6	31.7	921	9	AY293285	Mus muscu
30	267.6	30.8	921	6	CQ947408	Sequence
31	267.6	30.8	1250	6	CQ947429	Sequence
32	267.6	30.8	1276	6	CQ947433	Sequence
33	264.6	30.4	957	6	CQ947430	Sequence
34	264.6	30.4	1722	6	CQ947431	Sequence
35	258.8	29.7	927	9	AY590499	Rattus no
36	254.2	29.2	831	6	CQ947407	Sequence
37	236.8	27.2	750	6	CQ947406	Sequence
38	233	26.8	319	6	BD026702	Sequence
39	233	26.8	319	6	AX887092	Sequence
40	199.4	22.9	201	6	CQ947348	Sequence
41	198.4	22.8	201	6	CQ947361	Sequence
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43	157.2	18.1	537	6	CQ947437	Sequence
44	156.4	18.0	378	6	CQ947405	Sequence
45	149.2	17.1	540	6	CQ947400	Sequence

ALIGNMENTS

RESULT 1	AY293286	870 bp	mRNA	linear	PRI 18-JUN-2003
LOCUS	AY293286	Homo sapiens B and T lymphocyte attenuator (BTLA) mRNA, complete cds.			
DEFINITION	AY293286.1	GI:31880026			
ACCESSION	AY293286				
VERSION	AY293286.1				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 870)				
AUTHORS	Watanabe,N., Gavriel,M., Sedy,J.R., Yang,J., Yang,J., Fallarino,F., Loftin,S.K., Hurchla,M.A., Zimmerman,N., Sim,J., Zang,X., Murphy,T.L., Russell,J.H., Allison,J.P. and Murphy,K.M.				
TITLE	BTLA is a lymphocyte inhibitory receptor with similarities to CTLA-4 and PD-1				
JOURNAL	Nat. Immunol. (2003) In press				
REFERENCE	2 (bases 1 to 870)				
AUTHORS	Murphy,K.M., Watanabe,N., Yang,J. and Murphy,T.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-MAY-2003) Pathology, Washington University, 660 S. Euclid, St. Louis, MO 63110, USA				
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	/cell_line="Ramos"				
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CDS	1..870				
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	/product="B and T lymphocyte attenuator"				
	/protein_id="AAP44003.1"				
	/db_xref="GI:31880027"				

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 05:37:39 ; Search time 211 Seconds
(without alignments)
7329.283 Million cell updates/sec

Title: US-10-600-997-7

Perfect score: 870

Sequence: 1 atgaagacattgctgcat.....ccatattgtgaggagtaa 870

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/baCkfilese1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402.8	46.3	1903	3	US-09-369-247-39
2	402.8	46.3	1903	3	US-10-062-548-39
3	378	43.4	1940	3	US-09-369-247-58
4	378	43.4	1940	3	US-10-062-548-58
5	233	26.8	319	3	US-09-513-999C-2955
6	39.4	4.5	248968	3	US-09-949-016-12614
7	39.4	4.5	250958	3	US-09-949-016-16061
8	38	4.4	225127	3	US-09-949-016-16480
9	36.8	4.2	1137	3	US-09-543-681A-3307
10	36.6	4.2	832	3	US-09-621-976-2813
11	36.4	4.2	4305	3	US-09-645-593-1
12	36	4.1	832	3	US-09-621-976-2813
13	35.8	4.1	27425	3	US-09-524-101D-18
14	35.8	4.1	451924	3	US-09-949-016-12896
15	35.8	4.1	451925	3	US-09-949-016-17305
16	35.6	4.1	1664976	3	US-08-916-421B-1
17	35.6	4.1	1664976	3	US-09-692-570-1
18	35.4	4.1	2902	3	US-09-710-279-3489
19	35.4	4.1	235452	3	US-09-949-016-13675
20	34.8	4.0	88490	3	US-09-949-016-12758
21	34.8	4.0	88736	3	US-09-949-016-14222
22	34.4	4.0	399	3	US-09-621-976-8976
23	34.4	4.0	580073	3	US-08-545-528D-1
24	34.2	3.9	1191	3	US-09-107-532A-1085

25	34.2	3.9	1227	3	US-09-107-532A-3338	Sequence 3338, Ap
26	34.2	3.9	82612	3	US-09-949-016-16823	Sequence 16823, A
27	34.2	3.9	640681	3	US-09-790-988-1	Sequence 1, Appli
28	34	3.9	601	3	US-09-949-016-64746	Sequence 64746, A
29	34	3.9	57751	3	US-09-949-016-13631	Sequence 13631, A
30	33.8	3.9	1348	3	US-08-936-165A-186	Sequence 186, App
31	33.8	3.9	7218	2	US-08-232-463-14	Sequence 14, Appl
32	33.6	3.9	601	3	US-09-949-016-37431	Sequence 37431, A
33	33.6	3.9	601	3	US-09-949-016-195615	Sequence 195615, A
34	33.6	3.9	3001	3	US-09-539-333D-133	Sequence 133, App
35	33.6	3.9	94133	3	US-09-949-016-11901	Sequence 11901, A
36	33.6	3.9	94133	3	US-09-949-016-12713	Sequence 12713, A
37	33.6	3.9	94135	3	US-09-949-016-15934	Sequence 15934, A
38	33.6	3.9	94135	3	US-09-949-016-15935	Sequence 15935, A
39	33.6	3.9	94135	3	US-09-949-016-15936	Sequence 15936, A
40	33.6	3.9	94135	3	US-09-949-016-15937	Sequence 15937, A
41	33.6	3.9	110402	3	US-09-949-016-17295	Sequence 17295, A
42	33.6	3.9	110403	3	US-09-949-016-12741	Sequence 12741, A
43	33.6	3.9	1230025	3	US-09-198-452A-1	Sequence 1, Appli
44	33.6	3.9	1230230	3	US-09-438-185A-1	Sequence 1, Appli
45	33.4	3.8	991	3	US-09-270-767-2435	Sequence 2435, Ap

ALIGNMENTS

RESULT 1

US-09-369-247-39
; Sequence 39, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; EARLIER FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 1903
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-369-247-39

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Best Local Similarity	99.5%	Pred	No. 2.8e-110				
Mismatches	404	Conservative	0	Mismatches	2	Indels	0
Gaps	0						
QY	1	ATGAAGACATTCGCTGCCATCTTGGAACTGGGAATATTTTGGGTCTTCTTTAATC	60				
Db	52	ATGAAGACATTCGCTGCCATCTTGGAACTGGGAATATTTTGGGTCTTCTTTAATC	111				
QY	61	CCATATCTGGACATCTGGACATCCATCTAGCAGAGATCCCTTTGAACATGAGTGTACAGCTTTATATA	120				
Db	112	CCATATCTGGACATCTGGACATCCATCTAGCAGAGATCCCTTTGAACATGAGTGTACAGCTTTATATA	171				
QY	121	AAGACATCTGAACTCCATCTTAGCAGAGATCCCTTTGAACATGAGTGTACAGCTTTATATA	180				
Db	172	AAGACATCTGAACTCCATCTTAGCAGAGATCCCTTTGAACATGAGTGTACAGCTTTATATA	231				
QY	181	AAATATCTGTCTTAACAGGCTCATGTGCTTGGTCAAGCTCAATGGAAACAATGTGTA	240				
Db	232	AAATATCTGTCTTAACAGGCTCATGTGCTTGGTCAAGCTCAATGGAAACAATGTGTA	291				

QY 241 AAACCTTGAAGATAGACAAACAGTTTGAAGGAGAGAGAACATTTTCATTTTCAATCTA 300
 Db 292 AAACCTTGAAGATAGACAAACAGTTTGAAGGAGAGAGAACATTTTCATTTTCAATCTA 351
 QY 301 CATTTTGAACCAATGCTTCTTAATGACAAATGGGTGATACCGCTGTTCTGCAAAATTTTCAG 360
 Db 352 CATTTTGAACCAATGCTTCTTAATGACAAATGGGTGATACCGCTGTTCTGCAAAATTTTCAG 411
 QY 361 TCTAATCTCATTGAAAGCCACTCAACAACTCTTTATGTGACAGATG 406
 Db 412 TCTAATCTCATTGAAAGCCACTCAACAACTCTTTATGTGACAGGTG 457

RESULT 2
 US-10-062-548-39
 ; Sequence 39, Application US/10062548
 ; Patent No. 6924356
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 44 Human Secreted Proteins
 ; FILE REFERENCE: PZ024PI
 ; CURRENT APPLICATION NUMBER: US/10/062,548
 ; PRIOR FILING DATE: 2002-02-05
 ; PRIOR APPLICATION NUMBER: 09/369,247
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/074,118
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074,157
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074,137
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074,341
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074,141
 ; PRIOR FILING DATE: 1998-02-09
 ; NUMBER OF SEQ ID NOS: 172
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 39
 ; LENGTH: 1903
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-062-548-39

Query Match 46.3%; Score 402.8; DB 3; Length 1903;
 Best Local Similarity 99.5%; Pred. No. 2.8e-110;
 Matches 404; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Db 52 ATGAAGACATTCCTGCCATGCTTGAACCTGGGAATTTATTTGGGTCTTCTTTAAATC 111
 QY 61 CCATATCTGGACATCTGGAACATCCATGGGAAGAAATCATGTGATGATACAGCTTTATATA 120
 Db 112 CCATATCTGGACATCTGGAACATCCATGGGAAGAAATCATGTGATGATACAGCTTTATATA 171
 - QY 121 AAGAGACATCTGGAACATCTCCATCTTAGCAGGAGATCCCTTTGAACTAGAAATGCTGTG 180
 Db 172 AAGAGACATCTGGAACATCTCCATCTTAGCAGGAGATCCCTTTGAACTAGAAATGCTGTG 231
 QY 181 AAATCTGTGCTAAACAGGCTCATGTGACTTGTGCAAGCTCAATGGAACAAATGTTA 240
 Db 232 AAATCTGTGCTAAACAGGCTCATGTGACTTGTGCAAGCTCAATGGAACAAATGTTA 291
 QY 241 AAACCTTGAAGATAGACAAACAGTTTGAAGGAGAGAGAACATTTTCATTTTCAATCTA 300
 Db 292 AAACCTTGAAGATAGACAAACAGTTTGAAGGAGAGAGAACATTTTCATTTTCAATCTA 351
 QY 301 CATTTTGAACCAATGCTTCTTAATGACAAATGGGTGATACCGCTGTTCTGCAAAATTTTCAG 360
 Db 352 CATTTTGAACCAATGCTTCTTAATGACAAATGGGTGATACCGCTGTTCTGCAAAATTTTCAG 411
 QY 361 TCTAATCTCATTGAAAGCCACTCAACAACTCTTTATGTGACAGATG 406

Db 412 TCTAATCTCATTGAAAGCCACTCAACAACTCTTTATGTGACAGGTG 457
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 US-09-369-247-58
 ; Sequence 58, Application US/09369247
 ; Patent No. 6569992
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 44 Human Secreted Proteins
 ; FILE REFERENCE: PZ024PI
 ; CURRENT APPLICATION NUMBER: US/09/369,247
 ; CURRENT FILING DATE: 1999-08-05
 ; EARLIER APPLICATION NUMBER: 60/074,118
 ; EARLIER FILING DATE: 1998-02-09
 ; EARLIER APPLICATION NUMBER: 60/074,157
 ; EARLIER FILING DATE: 1998-02-09
 ; EARLIER APPLICATION NUMBER: 60/074,137
 ; EARLIER FILING DATE: 1998-02-09
 ; EARLIER APPLICATION NUMBER: 60/074,341
 ; EARLIER FILING DATE: 1998-02-09
 ; EARLIER APPLICATION NUMBER: 60/074,141
 ; EARLIER FILING DATE: 1998-02-09
 ; NUMBER OF SEQ ID NOS: 172
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 58
 ; LENGTH: 1940
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (5)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (1573)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-369-247-58

Query Match 43.4%; Score 378; DB 3; Length 1940;
 Best Local Similarity 98.5%; Pred. No. 7.5e-103;
 Matches 400; Conservative 2; Mismatches 2; Indels 2; Gaps 2;
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 Db 81 ATGAAGACATTCCTGCCATGCTTGAACCTGGGAATTTATTTGGGTCTTCTTTAAATC 140
 QY 61 CCATATCTGGACATCTGGAACATCCATGGGAAGAAATCATGTGATGATACAGCTTTATATA 120
 Db 141 CCATATCTGGACATCTGGAACATCCATGGGAAGAAATCATGTGATGATACAGCTTTATATA 200
 QY 121 AAGAGACATCTGGAACATCTCCATCTTAGCAGGAGATCCCTTTGAACTAGAAATGCTGTG 180
 Db 201 AAGAGACATCTGGAACATCTCCATCTTAGCAGGAGATCCCTTTGAACTAGAAATGCTGTG 260
 QY 181 AAATCTGTGCTAAACAGGCTCATGTGACTTGTGCAAGCTCAATGGAACAAATGTTA 240
 Db 261 AAATCTGTGCTAAACAGGCTCATGTGACTTGTGCAAGCTCAATGGAACAAATGTTA 320
 QY 241 AAACCTTGAAGATAGACAAACAGTTTGAAGGAGAGAGAACATTTTCATTTTCAATCTA 300
 Db 321 AAACCTTGAAGATAGACAAACAGTTTGAAGGAGAGAGAACATTTTCATTTTCAATCTA 378
 QY 301 CATTTTGAACCAATGCTTCTTAATGACAAATGGGTGATACCGCTGTTCTGCAAAATTTTCAG 360
 Db 379 CATTTTGAACCAATGCTTCTTAATGACAAATGGGTGATACCGCTGTTCTGCAAAATTTTCAG 438
 QY 361 TCTAATCTCATTGAAAGCCACTCAACAACTCTTTATGTGACAGATG 406
 Db 439 TCTAATCTCATTGAAAGCCACTCAACAACTCTTTATGTGACAGGTG 484

GenCore version 5.1.7
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(without alignments)
561.171 Million cell updates/sec

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Searched: 6240305 seqs, 449581930 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US17_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854	98.2	1066	7	US-10-987-663-1
2	829.2	95.3	888	7	US-10-987-663-9
3	564	64.8	726	7	US-10-987-663-7
4	36.8	4.2	1923	7	US-10-750-185-43526
5	36.8	4.2	1923	7	US-10-750-185-43526
6	36.8	4.2	147700	7	US-10-857-780-3
7	35.6	4.1	598	7	US-10-750-185-3972
8	35.6	4.1	598	7	US-10-750-185-3972
9	35.4	4.1	2902	7	US-10-793-626-3489
10	35	4.0	2884	7	US-10-750-185-27365
11	35	4.0	2884	7	US-10-750-185-27365
12	34.4	4.0	611587	11	US-11-117-187-209
13	34.2	3.9	1151	7	US-10-750-185-38526
14	34.2	3.9	1151	7	US-10-750-185-38526
15	34.2	3.9	1980	7	US-10-750-185-29535
16	34.2	3.9	1980	7	US-10-750-185-29535
17	34.2	3.9	1457619	11	US-11-098-686-8739
18	33.8	3.9	585	11	US-11-136-527-40
19	33.8	3.9	585	11	US-11-136-527-40
20	33.6	3.9	1217	7	US-10-750-185-41654
21	33.6	3.9	1217	7	US-10-750-185-41654

c	22	33.6	3.9	1402	7	US-10-750-185-38574	Sequence 38574, A
c	23	33.6	3.9	1402	7	US-10-750-623-38574	Sequence 38574, A
c	24	33.6	3.9	3001	11	US-11-145-703-133	Sequence 133, App
c	25	33.6	3.9	5439	7	US-10-750-185-63066	Sequence 63066, A
c	26	33.6	3.9	5439	7	US-10-750-623-63066	Sequence 63066, A
c	27	33.6	3.9	165627	11	US-11-121-086-89	Sequence 89, Appl
c	28	33.2	3.8	1589	7	US-10-750-185-35617	Sequence 35617, A
c	29	33.2	3.8	1589	7	US-10-750-623-35617	Sequence 35617, A
c	30	33	3.8	1400	11	US-11-136-527-7444	Sequence 7444, Ap
c	31	33	3.8	1692	11	US-11-136-527-3348	Sequence 3348, Ap
c	32	33	3.8	6113	7	US-10-240-708-14	Sequence 14, Appl
c	33	33	3.8	7872	11	US-11-136-527-23235	Sequence 23235, Ap
c	34	33	3.8	340000	11	US-11-102-978-3	Sequence 3, Appl
c	35	32.8	3.8	159138	7	US-10-995-561-13230	Sequence 13230, A
c	36	32.6	3.7	949	7	US-10-750-185-34489	Sequence 34489, A
c	37	32.6	3.7	949	7	US-10-750-623-34489	Sequence 34489, A
c	38	32.6	3.7	952	7	US-10-750-185-28945	Sequence 28945, A
c	39	32.6	3.7	952	7	US-10-750-623-28945	Sequence 28945, A
c	40	32.4	3.7	1941	7	US-10-750-185-26450	Sequence 26450, A
c	41	32.4	3.7	1941	7	US-10-750-623-26450	Sequence 26450, A
c	42	32.4	3.7	2467	7	US-10-750-185-29248	Sequence 29248, A
c	43	32.4	3.7	2467	7	US-10-750-623-29248	Sequence 29248, A
c	44	32.4	3.7	188056	11	US-11-120-925-1	Sequence 1, Appl
c	45	32.2	3.7	201	7	US-10-995-561-6891	Sequence 6891, Ap

ALIGNMENTS

RESULT 1
US-10-987-663-1
; Sequence 1, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LENGTH: 1066
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-987-663-1

Query Match 98.2%; Score 854; DB 7; Length 1066;
Best Local Similarity 98.9%; Pred. No. 4.5e-233;
Matches 860; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	1	ATGAAGACATTCGCTGCCATGCTTGGAACTGGGAATATTTTGGGTCTTCTTTAATC	60
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QY	61	CCATATCTGGACATCTGGAACTCCATCGGAAAGAAATCATGTGATGATACAGCTTTATATA	120
DB	84	CCATATCTGGACATCTGGAACTCCATCGGAAAGAAATCATGTGATGATACAGCTTTATATA	143
QY	121	AGAGACATCTGAACTCCATCTTAGCAGAGATCCCTTTGAACATAGATGCCCTGTG	180
DB	144	AGAGACATCTGAACTCCATCTTAGCAGAGATCCCTTTGAACATAGATGCCCTGTG	203

GenCore version 5.1.7
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Run on: February 10, 2006, 05:30:15 ; Search time 3747 Seconds
(without alignments)
10863.294 Million cell updates/sec

Title: US-10-600-997-7

Perfect score: 870

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Scoring table: IDENTITY NUC

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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gsa1:*

10: gb_gsa2:*

11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469.6	54.0	483	5	BX111230 BX111230
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4	314.4	36.1	488	1	AI792952 om87f10.y
5	289.6	33.3	478	1	AI651719 wb26a04.x
6	270.6	31.1	3229	4	AK041334 Mus muscu
7	257.2	29.6	444	1	AW188302 xj9sa02.x
8	256.2	29.4	443	1	AW241471
9	254	29.2	445	2	BF940033
10	242.8	27.9	428	1	AW241411
11	185	21.3	763	7	CO558897
12	156.2	18.0	693	2	BB638002
13	155.6	17.9	517	7	CN680177
14	138.8	16.0	633	2	BE306748
15	136	15.6	311	1	AA931122
16	131.6	15.1	611	7	CO571762
17	126.8	14.6	855	9	BZ102470
18	123.4	14.2	599	11	CR049292
19	118.8	13.7	478	1	AI235902
20	111.8	12.9	502	2	BF661404
21	91.2	10.5	396	7	CR474407
22	72	8.3	748	6	CB963019

23	64.2	7.4	153	2	BE832323
24	58	6.7	570	11	CR865259
25	57	6.6	815	9	BZ273233
26	51.6	5.9	551	10	CG991478
27	45.4	5.2	4756	4	CR857077
28	42	4.8	777	9	BZ080723
29	40.6	4.7	423	8	T09379
30	40.6	4.7	460	1	AI632280
31	40.6	4.7	461	1	AI654788
32	40.6	4.7	473	1	AI204353
33	40.6	4.7	500	3	BM150540
34	40.6	4.7	500	3	BM782571
35	40.6	4.7	501	6	CB135481
36	40.6	4.7	504	2	BF195894
37	40.6	4.7	522	1	AI961504
38	40.6	4.7	542	3	BI966027
39	40.6	4.7	549	2	BE348610
40	40.6	4.7	549	6	CA868466
41	40.6	4.7	573	2	BF111119
42	40.6	4.7	579	3	BM829805
43	40.6	4.7	580	3	BM021328
44	40.6	4.7	586	1	AI829721
45	40.6	4.7	587	3	BM021090

ALIGNMENTS

RESULT 1
BX111230
LOCUS
DEFINITION
BX111230 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE2306766, mRNA sequence.
ACCESSION
BX111230
VERSION
BX111230.1 GI:27836886
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 483)
AUTHORS
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
TITLE
Human Unigeneset - RZPD3
JOURNAL
Unpublished (2003)
COMMENT
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE2306766
RZPDLIB, I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTTACACGAGAACAGCTATGAC.
Location/Qualifiers
1. .483
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE2306766"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"
/note="Vector: pTT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA

source

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 16:43:11 ; Search time 143 Seconds
(without alignments)
887.975 Million cell updates/sec

Title: US-10-600-997-8

Perfect score: 1557

Sequence: 1 MKTFLPMLGTGKLFVFFLI.....RLRNVKCAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003s.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1557	100.0	289	ADH34662	Adh34662 Human BTL
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3	1516	97.4	289	ADH34661	Adh34661 Human BTL
4	1516	97.4	289	ADH34661	Adh34661 Human BTL
5	1516	97.4	289	ADH34661	Adh34661 Human BTL
6	1516	97.4	289	ADH34661	Adh34661 Human BTL
7	1516	97.4	289	ADH34661	Adh34661 Human BTL
8	1509	96.9	289	ADH34661	Adh34661 Human BTL
9	1479	95.0	283	ADH34661	Adh34661 Human BTL
10	1347	86.5	259	ADH34661	Adh34661 Human BTL
11	1246	80.0	239	ADH34661	Adh34661 Human BTL
12	1239	79.6	241	ADH34661	Adh34661 Human BTL
13	1239	79.6	241	ADH34661	Adh34661 Human BTL
14	981	63.0	194	ADH34661	Adh34661 Human BTL
15	958	61.5	178	ADH34661	Adh34661 Human BTL
16	849	54.5	157	ADH34661	Adh34661 Human BTL
17	819	52.6	390	ADH34661	Adh34661 Human BTL
18	789	50.7	148	ADH34661	Adh34661 Human BTL
19	741.5	47.6	212	ADH34661	Adh34661 Human BTL
20	741.5	47.6	212	ADH34661	Adh34661 Human BTL
21	741.5	47.6	212	ADH34661	Adh34661 Human BTL
22	723.5	46.5	306	ADH34661	Adh34661 Human BTL
23	719.5	46.2	306	ADH34661	Adh34661 Human BTL
24	719.5	46.2	538	ADH34661	Adh34661 Human BTL

25	680	43.7	127	8	ADU51061	ADU51061 Human SPE
26	667	42.8	132	8	ADU51067	ADU51067 Human SPE
27	653.5	42.0	277	8	ADU51111	ADU51111 Murine sp
28	615.5	39.5	250	8	ADU51110	ADU51110 Murine sp
29	558	35.8	111	8	ADU51066	ADU51066 Human BTL
30	540	34.7	98	9	AE92075	AE92075 Human BTL
31	516	33.1	101	6	ADA57590	ADA57590 Human sec
32	516	33.1	101	6	ADA41487	ADA41487 Human sec
33	516	33.1	102	2	AAV30859	AAV30859 Human sec
34	458	28.4	204	8	ADU51106	ADU51106 Murine sp
35	440	28.3	78	3	AG02951	AG02951 Human sec
36	405	26.0	179	8	ADU51134	ADU51134 Murine sp
37	405	26.0	411	8	ADU51149	ADU51149 Spleen-ex
38	394	25.3	180	8	ADU51104	ADU51104 Murine sp
39	392	25.2	175	8	ADU51105	ADU51105 Murine sp
40	374	24.0	65	8	ADU51052	ADU51052 Human spl
41	341	21.9	67	8	ADU51065	ADU51065 Human SPE
42	339	21.8	150	8	ADU51135	ADU51135 Murine SP
43	328	21.1	151	8	ADU51103	ADU51103 Murine SP
44	326	20.9	126	8	ADU51109	ADU51109 Murine SP
45	261.5	16.8	102	8	ADU51108	ADU51108 Murine sp

ALIGNMENTS

RESULT 1
ADH34662
ID ADH34662 standard; protein; 289 AA.

AC ADH34662;

DT 11-MAR-2004 (first entry)

DE Human BTLA.

B7x; ligand; B and T lymphocyte attenuator; BTLA; tumour; inhibition;
tumour-specific; immunological tolerance; cancer; autoimmune disease;
diabetes; pre-eclampsia; rheumatoid arthritis; multiple sclerosis;
infection; graft rejection; cell cycle progression; differentiation;
survival; cytokine production; cytolytic activation;
antigen presentation; antibody production.

OS Homo sapiens.

Key Location/Qualifiers

Peptide /note= "Signal peptide"

Disulfide-bond /note= "Disulphide bond"

Modified-site /note= "Glycosylated"

Domain /note= "Transmembrane domain"

Region /note= "Conserved sequence"

Region /note= "Conserved sequence"

Region /note= "Conserved sequence"

WO2004000221-A2.

31-DEC-2003.

20-JUN-2003; 2003WO-US019614.

20-JUN-2002; 2002US-0390653P.

06-JAN-2003; 2003US-0438593P.

(REGC) UNIV CALIFORNIA.

(UNIW) UNIV WASHINGTON.

PI Allison JP, Murphy KP, Watanabe N, Murphy TL, Yang J, Zang X;
 XX WPI; 2004-082409/08.
 XX New recombinant B and T lymphocyte attenuator nucleic acid and protein,
 PT useful for modulating B and T lymphocyte activity, or for diagnosing and
 PT treating cancer, autoimmune disease or infectious disease.
 XX Claim 81; Fig 28; 121pp; English.
 CC This sequence represents a human B and T lymphocyte attenuator (BTLA).
 CC BTLA acts as a negative regulator of both B and T lymphocyte activity,
 CC where signaling mediated by BTLA results in the inhibition of BTLA-
 CC positive lymphocyte activity. In BTLA-positive T cells BTLA signalling
 CC can inhibit TCR-induced T cell responses, such as cell cycle progression,
 CC differentiation, survival, cytokine production and cytolytic activation.
 CC In BTLA-positive B cells BTLA signalling can inhibit B cell antigen
 CC receptor-induced B cell responses, such as cell cycle progression,
 CC differentiation, survival, antigen presentation and antibody production.
 CC B7x is a ligand for the recombinant BTLA of the invention. B7x is able to
 CC negatively regulate B and T lymphocyte activity through its interaction
 CC with BTLA, which inhibits both B and T cell responses. Therefore B7x
 CC positive tumour tissue inhibits the activity of tumour-specific T cells.
 CC B7x is also expressed on non-tumour non-lymphoid tissue, showing that the
 CC B7x/BTLA interaction is a mechanism for maintaining immunological
 CC tolerance. BTLA proteins and related nucleic acids are useful for
 CC modulating B and T lymphocyte activity, for diagnosing and treating
 CC cancer, autoimmune disease, e.g. diabetes, pre-eclampsia, rheumatoid
 CC arthritis or multiple sclerosis, or infectious disease, or for preventing
 CC acute and/or chronic graft rejection.
 XX Sequence '289 AA;
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Query Match 100.0%; Score 1557; DB 8; Length 289;
 Best Local Similarity 100.0%; Pred. No. 5.2e-140;
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTLPAMLTGKLFVWFFLIPYLDIWNHKGKSCDVLKQSEHSILAGDPFLECPV 60
 DB 1 MKTLPAMLTGKLFVWFFLIPYLDIWNHKGKSCDVLKQSEHSILAGDPFLECPV 60

QY 61 KYCANRPHVTWCKLNGTTCVKLEDROTWSKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
 DB 61 KYCANRPHVTWCKLNGTTCVKLEDROTWSKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120

QY 121 SNLIESHSYTLVTDVKGASRPSKDEVASRPMWLSYLLPLGLPLLIITWFCFLCCLR 180
 DB 121 SNLIESHSYTLVTDVKGASRPSKDEVASRPMWLSYLLPLGLPLLIITWFCFLCCLR 180

QY 181 HQGKQNELSDTAGREINLVDAHLKSEQTASTRONSQVLLSEAGIYDNDPDLCFRMOEGS 240
 DB 181 HQGKQNELSDTAGREINLVDAHLKSEQTASTRONSQVLLSEAGIYDNDPDLCFRMOEGS 240

QY 241 EVCNPNCLSENKPGIYVYASLNHNSVIGLSRLRNKVEAPTEYASICVRS 289
 DB 241 EVCNPNCLSENKPGIYVYASLNHNSVIGLSRLRNKVEAPTEYASICVRS 289

RESULT 2
 ADH34661
 ID ADH34661 standard; protein; 289 AA.
 XX ADH34661;
 AC ADH34661;
 XX 11-MAR-2004 (first entry)
 DT Human BTLA.
 DE B7x; ligand; B and T lymphocyte attenuator; BTLA; tumour; inhibition;
 XX tumour-specific; immunological tolerance; cancer; autoimmune disease;
 KW diabetes; pre-eclampsia; rheumatoid arthritis; multiple sclerosis;
 KW infection; graft rejection; cell cycle progression; differentiation;
 KW survival; cytokine production; cytolytic activation;

KW antigen presentation; antibody production.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..28
 FT /note= "Signal peptide"
 FT Disulfide-bond 58..115
 FT /note = Disulphide bond
 FT Modified-site 110
 FT /note= "Glycosylated"
 FT Domain 154..182
 FT /note = Transmembrane domain
 FT Region 223..229
 FT /note= "Conserved sequence"
 FT Region 254..262
 FT /note= "Conserved sequence"
 FT Region 277..289
 FT /note= "Conserved sequence"
 XX WO2004000221-A2.
 PN 31-DEC-2003.
 PD 20-JUN-2003; 2003WO-US019614.
 XX 20-JUN-2003; 2002US-0390653P.
 PR 06-JAN-2003; 2003US-0438593P.
 XX (REGC) UNIV CALIFORNIA.
 PA (UNIW) UNIV WASHINGTON.
 XX Allison JP, Murphy KP, Watanabe N, Murphy TL, Yang J, Zang X;
 PI WPI; 2004-082409/08.
 DR New recombinant B and T lymphocyte attenuator nucleic acid and protein,
 PT useful for modulating B and T lymphocyte activity, or for diagnosing and
 PT treating cancer, autoimmune disease or infectious disease.
 XX Example 4; Fig 19; 121pp; English.
 PS This sequence represents a human B and T lymphocyte attenuator (BTLA).
 XX BTLA acts as a negative regulator of both B and T lymphocyte activity,
 CC where signaling mediated by BTLA results in the inhibition of BTLA-
 CC positive lymphocyte activity. In BTLA-positive T cells BTLA signalling
 CC can inhibit TCR-induced T cell responses, such as cell cycle progression,
 CC differentiation, survival, cytokine production and cytolytic activation.
 CC In BTLA-positive B cells BTLA signalling can inhibit B cell antigen
 CC receptor-induced B cell responses, such as cell cycle progression,
 CC differentiation, survival, antigen presentation and antibody production.
 CC B7x is a ligand for the recombinant BTLA of the invention. B7x is able to
 CC negatively regulate B and T lymphocyte activity through its interaction
 CC with BTLA, which inhibits both B and T cell responses. Therefore B7x
 CC positive tumour tissue inhibits the activity of tumour-specific T cells.
 CC B7x is also expressed on non-tumour non-lymphoid tissue, showing that the
 CC B7x/BTLA interaction is a mechanism for maintaining immunological
 CC tolerance. BTLA proteins and related nucleic acids are useful for
 CC modulating B and T lymphocyte activity, for diagnosing and treating
 CC cancer, autoimmune disease, e.g. diabetes, pre-eclampsia, rheumatoid
 CC arthritis or multiple sclerosis, or infectious disease, or for preventing
 CC acute and/or chronic graft rejection.
 XX Sequence 289 AA;
 SQ

Query Match 97.4%; Score 1516; DB 8; Length 289;
 Best Local Similarity 97.9%; Pred. No. 4.3e-136;
 Matches 289; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKTLPAMLTGKLFVWFFLIPYLDIWNHKGKSCDVLKQSEHSILAGDPFLECPV 60
 DB 1 MKTLPAMLTGKLFVWFFLIPYLDIWNHKGKSCDVLKQSEHSILAGDPFLECPV 60

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OM protein - protein search, using sw model

Run on: February 8, 2006, 16:54:56 ; Search time 118.5 Seconds
(without alignments)
1019.010 Million cell updates/sec

Title: US-10-600-997-8
Perfect score: 1557
Sequence: 1 MKTLPAMLGKGLFWFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1516	97.4	289	4	US-10-371-341-2
3	1516	97.4	289	4	US-10-600-997-6
4	1516	97.4	289	5	US-10-831-622-21
5	1516	97.4	289	5	US-10-964-215-21
6	1516	97.4	289	5	US-10-989-826-28
7	1516	97.4	521	5	US-10-831-622-98
8	1516	97.4	521	5	US-10-964-215-98
9	1347	86.5	259	5	US-10-831-622-20
10	1347	86.5	259	5	US-10-964-215-20
11	1246	80.0	239	5	US-10-831-622-19
12	1246	80.0	239	5	US-10-964-215-19
13	1239	79.6	241	4	US-10-471-449-10
14	958	61.5	178	5	US-10-831-622-15
15	958	61.5	178	5	US-10-964-215-15
16	849	54.5	157	5	US-10-831-622-13
17	849	54.5	157	5	US-10-964-215-13
18	789	50.7	148	5	US-10-831-622-14
19	789	50.7	148	5	US-10-964-215-14
20	741.5	47.6	212	4	US-10-062-548-88
21	741.5	47.6	212	5	US-10-918-446-88
22	741.5	47.6	212	6	US-11-002-755-88
23	741.5	47.6	212	6	US-11-002-756-88
24	723.5	46.5	306	4	US-10-600-997-5
25	723.5	46.5	306	4	US-10-600-997-10
26	719.5	46.2	306	5	US-10-831-622-63
27	719.5	46.2	306	5	US-10-964-215-63

ALIGNMENTS

RESULT 1

US-10-600-997-8
; Sequence 8, Application US/10600997
; Publication No. US20040175380A1
; GENERAL INFORMATION:
; APPLICANT: Allison, James
; APPLICANT: Murphy, Kenneth
; APPLICANT: Watanabe, Norihiko
; APPLICANT: Murphy, Theresa
; APPLICANT: Yang, Jianfei
; APPLICANT: Zang, Xingxing
; TITLE OF INVENTION: Compositions and Methods for Modulating Lymphocyte Activity
; FILE REFERENCE: A-71608/TAL/DHR
; CURRENT APPLICATION NUMBER: US/10/600,997
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/390,653
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/438,593
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-600-997-8

Query Match	100.0%	Score 1557;	DB 4;	Length 289;
Best Local Similarity	100.0%	Pred. No. 1e-149;	Mismatches 0;	Indels 0;
Matches 289;	Conservative 0;			Gaps 0;
QY	1	MKTLPAMLGKGLFWFFLI	PYDITWNIHGKESCDVQLYIKRQSHSILAGDPFELECPV	60
Db	1	MKTLPAMLGKGLFWFFLI	PYDITWNIHGKESCDVQLYIKRQSHSILAGDPFELECPV	60
QY	61	KYCANRPHVTWCKLNGTT	CVKLEDRQTSWKEKNISPFILHPEPMLPNDNGSYRCSANFQ	120
Db	61	KYCANRPHVTWCKLNGTT	CVKLEDRQTSWKEKNISPFILHPEPMLPNDNGSYRCSANFQ	120
QY	121	SNLTESHSTTLYVTDVKASRPSKDE	VASRPWLLYSLLPLGGLPILLITWTFCLCCLRR	180
Db	121	SNLTESHSTTLYVTDVKASRPSKDE	VASRPWLLYSLLPLGGLPILLITWTFCLCCLRR	180
QY	181	HQKQNELSDTAGREINLVDAHLKSE	QTEASTRONSQVLLSEAGIYDNDPDLCFRMOEGS	240
Db	181	HQKQNELSDTAGREINLVDAHLKSE	QTEASTRONSQVLLSEAGIYDNDPDLCFRMOEGS	240
QY	241	EVCNSNPLEENKPGIVYASLNHSV	TGLNSRLARNVKEAPTEYASICVRS	289
Db	241	EVCNSNPLEENKPGIVYASLNHSV	TGLNSRLARNVKEAPTEYASICVRS	289

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OM protein - protein search, using sw model

Run on: February 8, 2006, 16:54:06 ; Search time 34.5 Seconds
(without alignments)
692.559 Million cell updates/sec

Title: US-10-600-997-8
Perfect score: 1557
Sequence: 1 MKTLPAMLTGKLFVFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2.6/prodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2.6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2.6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741.5	47.6	212	2	US-09-369-247-88
2	741.5	47.6	212	2	US-10-062-548-88
3	516	33.1	102	2	US-09-369-247-107
4	516	33.1	102	2	US-10-062-548-107
5	440	28.3	78	2	US-09-513-999C-7032
6	121.5	7.8	343	1	US-08-348-792-10
7	121.5	7.8	343	1	US-08-462-738-10
8	121.5	7.8	343	2	US-09-199-955-10
9	121.5	7.8	343	2	US-08-880-875-10
10	117	7.5	1953	2	US-09-917-254-92
11	115	7.4	624	1	US-08-642-406A-22
12	115	7.4	624	2	US-09-199-534-22
13	115	7.4	624	2	US-09-199-534-22
14	115	7.4	624	2	US-09-491-322-22
15	115	7.4	773	2	US-08-434-000A-2
16	115	7.4	773	2	US-09-312-157-2
17	115	7.4	773	2	US-09-717-888-2
18	115	7.4	773	2	US-09-818-247-6
19	101.5	6.5	329	1	US-08-348-792-12
20	101.5	6.5	329	1	US-08-462-738-12
21	101.5	6.5	329	2	US-09-199-955-12
22	101.5	6.5	329	2	US-08-880-875-12
23	98.5	6.3	278	2	US-09-270-767-42034
24	97.5	6.3	119	2	US-09-858-664A-30
25	97.5	6.3	119	2	US-10-274-978-31
26	97.5	6.3	119	2	US-10-697-263-31
27	97.5	6.3	766	2	US-09-854-845-49

28	97.5	6.3	771	2	US-09-854-845-47	Sequence 47, Appl
29	97.5	6.3	865	2	US-09-854-845-33	Sequence 33, Appl
30	97.5	6.3	870	2	US-09-854-845-31	Sequence 31, Appl
31	95.5	6.1	739	2	US-09-854-845-45	Sequence 45, Appl
32	95.5	6.1	744	2	US-09-854-845-43	Sequence 43, Appl
33	95.5	6.1	838	2	US-09-854-845-29	Sequence 29, Appl
34	95.5	6.1	843	2	US-09-854-845-27	Sequence 27, Appl
35	94	6.0	771	1	US-08-742-753-2	Sequence 2, Appl
36	93.5	6.0	622	2	US-09-499-846-2	Sequence 8, Appl
37	93	6.0	921	1	US-08-568-459A-8	Sequence 8, Appl
38	93	6.0	921	1	US-08-487-826B-8	Sequence 8, Appl
39	93	6.0	921	2	US-09-210-288-8	Sequence 8, Appl
40	93	6.0	921	2	US-10-153-273-8	Sequence 8, Appl
41	90.5	5.8	283	2	US-09-904-615-106	Sequence 106, App
42	90.5	5.8	283	2	US-10-054-988-106	Sequence 106, App
43	90	5.8	780	1	US-08-232-538-14	Sequence 14, Appl
44	90	5.8	780	1	US-08-786-164-14	Sequence 14, Appl
45	90	5.8	1311	1	US-08-340-011-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-369-247-88
; Sequence 88, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-369-247-88

Query Match 47.6%; Score 741.5; DB 2; Length 212;
Best Local Similarity 94.4%; Pred. No. 3.4e-69;
Matches 136; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
QY 1 MKTLPAMLTGKLFVFFLIPLYLDIWNHKGSCDVLVIKQSEHSILAGDPFELECPV 60
Db 1 MKTLPAMLTGKLFVFFLIPLYLDIWNHKGSCDVLVIKQSEHSILAGDPFELECPV 60
QY 61 KYCANRPHVTVCKLNGTTTCVKLEDQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
Db 61 KYCANRPHVTVCKLNGTTTCVKLEDQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
QY 121 SNLIESHTTLYVTVKGSERPS 144
Db 121 SNLIESHTTLYVTG-EFSTPRPS 143

RESULT 2
US-10-062-548-88
; Sequence 88, Application US/10062548
; Patent No. 6924356
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 44 Human Secreted Proteins
 ; FILE REFERENCE: P2024P1
 ; CURRENT APPLICATION NUMBER: US/10/062,548
 ; CURRENT FILING DATE: 2002-02-05
 ; PRIOR APPLICATION NUMBER: 09/369,247
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/074,118
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074,157
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074,137
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074,341
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074,141
 ; PRIOR FILING DATE: 1998-02-09
 ; NUMBER OF SEQ ID NOS: 172
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 88
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-062-548-88

Query Match 47.6%; Score 741.5; DB 2; Length 212;
 Best Local Similarity 94.4%; Pred. No. 3.4e-69;
 Matches 136; Conservative 4; Mismatches 3; Indels 1; Gaps 1

QY 1 MXTLPAMLTGKLFWVFLIPLYDINWJHGKSCDVQLYIKROSEHSILAGDPFLECPV 60
 Db 1 MXTLPAMLTGKLFWVFLIPLYDINWJHGKSCDVQLYIKROSEHSILAGDPFLECPV 60
 QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISPFILHFPMLPNDNGSYRCSANFQ 120
 Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISPFILHFPMLPNDNGSYRCSANFQ 120
 QY 121 SNLIESHSTLYLVTDVKGASRPS 144
 Db 121 SNLIESHSTLYLVTDVKGASRPS 143

RESULT 3
 US-09-369-247-107
 ; Sequence 107, Application US/09369247
 ; Patent No. 6569922
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 44 Human Secreted Proteins
 ; FILE REFERENCE: P2024P1
 ; CURRENT APPLICATION NUMBER: US/09/369,247
 ; CURRENT FILING DATE: 1999-08-05
 ; EARLIER APPLICATION NUMBER: 60/074,118
 ; EARLIER FILING DATE: 1998-02-09
 ; EARLIER APPLICATION NUMBER: 60/074,157
 ; EARLIER FILING DATE: 1998-02-09
 ; EARLIER APPLICATION NUMBER: 60/074,137
 ; EARLIER FILING DATE: 1998-02-09
 ; EARLIER APPLICATION NUMBER: 60/074,341
 ; EARLIER FILING DATE: 1998-02-09
 ; EARLIER APPLICATION NUMBER: 60/074,141
 ; EARLIER FILING DATE: 1998-02-09
 ; NUMBER OF SEQ ID NOS: 172
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 107
 ; LENGTH: 102
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (101)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; FEATURE:

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:56:11 ; Search time 10 Seconds
(without alignments)
379,241 Million cell updates/sec

Title: US-10-600-997-8
Perfect score: 1557
Sequence: 1 MKTLPAMLTGKLFVFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 1312538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:
1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pap:
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pap:
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pap:
4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pap:
5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pap:
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pap:
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pap:
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1516	97.4	289	6	US-10-987-663-2
2	1503	96.5	295	6	US-10-987-663-10
3	1239	79.6	241	6	US-10-987-663-8
4	90.5	5.8	822	7	US-11-183-567A-2
5	90	5.8	1338	7	US-11-109-156-23
6	90	5.8	3588	6	US-10-995-561-672
7	90	5.8	4346	6	US-10-995-561-671
8	90	5.8	4347	6	US-10-995-561-670
9	90	5.8	4390	6	US-11-169-041-169
10	90	5.8	4419	6	US-10-821-234-1155
11	89	5.7	4495	6	US-10-453-372-1002
12	89	5.7	5636	7	US-11-065-695-20
13	88	5.7	244	7	US-11-156-084-218
14	87	5.6	2828	7	US-11-080-991-54
15	87	5.6	2828	7	US-11-186-284-49
16	86	5.5	1338	6	US-10-821-234-1622
17	85.5	5.5	976	7	US-11-148-770-31
18	85.5	5.5	1150	7	US-11-139-435-1
19	85	5.5	534	6	US-10-821-234-1341
20	84	5.4	235	6	US-10-453-372-784
21	84	5.4	284	6	US-10-453-372-790
22	84	5.4	290	6	US-10-453-372-776
23	84	5.4	302	6	US-10-453-372-780
24	84	5.4	302	6	US-10-453-372-782
25	84	5.4	302	6	US-10-453-372-788

26	84	5.4	458	6	US-10-453-372-786	Sequence 786, App
27	84	5.4	464	6	US-10-453-372-772	Sequence 772, App
28	84	5.4	464	6	US-10-453-372-774	Sequence 774, App
29	84	5.4	473	6	US-10-453-372-770	Sequence 770, App
30	83.5	5.4	205	7	US-11-000-463-863	Sequence 863, App
31	82.5	5.3	234	7	US-10-927-322-1	Sequence 1, Appli
32	81.5	5.2	7968	7	US-11-186-731-5	Sequence 5, Appli
33	81	5.2	136	7	US-11-156-084-324	Sequence 324, App
34	81	5.2	399	7	US-11-159-919-4	Sequence 4, Appli
35	81	5.2	758	7	US-11-043-693-1	Sequence 1, Appli
36	80.5	5.2	305	7	US-11-000-463-391	Sequence 391, App
37	80.5	5.2	842	7	US-11-124-368A-171	Sequence 171, App
38	80.5	5.2	1191	7	US-11-139-435-2	Sequence 2, Appli
39	80	5.1	302	6	US-10-453-372-792	Sequence 792, App
40	79.5	5.1	148	7	US-11-147-047-28	Sequence 28, Appl
41	79	5.1	236	7	US-11-000-463-862	Sequence 862, App
42	78.5	5.0	1193	7	US-11-139-435-3	Sequence 3, Appli
43	78	5.0	309	6	US-10-453-372-778	Sequence 778, App
44	78	5.0	900	7	US-11-144-987-4	Sequence 4, Appli
45	78	5.0	902	7	US-11-144-987-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-987-663-2
; Sequence 2, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: CUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-2

Query Match	97.4%	Score 1516;	DB 6;	Length 289;
Best Local Similarity	97.9%	Pred. No. 7.1e-139;		
Matches 283;	Conservative 2;	Mismatches 4;	Indels 0;	Gaps 0;
QY	1	MKTLPAMLTGKLFVFFLI	PYLDIWNTHGKSCDVLYIKQSEHSILAGDPPELECPV	60
DB	1	MKTLPAMLTGKLFVFFLI	PYLDIWNTHGKSCDVLYIKQSEHSILAGDPPELECPV	60
QY	61	KYCANRPHVTWCKLNGTTGVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSVYRCSANFQ	120	
DB	61	KYCANRPHVTWCKLNGTTGVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSVYRCSANFQ	120	
QY	121	SNLIESHTTLYVTDVKGASERPSKDEVASRPWLYSLPLGLGLPLLIITWTFCLFCLRR	180	
DB	121	SNLIESHTTLYVTDVKGASERPSKDEMASRPWLYSLPLGLGLPLLIITWTFCLFCLRR	180	
QY	181	HQKQNELSDTAGRINLVDAHLKSEQTEASTRQNSQVLLSAGIYDNDPDLICFRMQEBS	240	
DB	181	HQKQNELSDTAGRINLVDAHLKSEQTEASTRQNSQVLLSAGIYDNDPDLICFRMQEBS	240	

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QY 241 EYVSNPCLEENKPGIYVYASLNHSGVGLNSRLARNVKEAPTEYASICVRS 289
|||
Db 241 EYVSNPCLEENKPGIYVYASLNHSGVGLNSRLARNVKEAPTEYASICVRS 289
|||

RESULT 2
US-10-987-663-10
; Sequence 10, Application US/10987663
; Publication NO. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY L.
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-10

Query Match 96.5%; Score 1503; DB 6; Length 295;
Best Local Similarity 95.9%; Pred. No. 1.3e-137;
Matches 283; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 MKTLPAMLTGKLFVWFVFLIPYLDIWNHSGKSCDVLYIKRQSEHSILAGDPFPELECPV 60
|||
Db 1 MKTLPAMLTGKLFVWFVFLIPYLDIWNHSGKSCDVLYIKRQSEHSILAGDPFPELECPV 60
|||

QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
|||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
|||

QY 121 SNLIESHTTLYVT-----DVKGASERSKDEVASRPMWLLYSLPLGLPLLTITWFC 174
|||
Db 121 SNLIESHTTLYVTAFNTIPDVKSASERSKDEMASRPMWLLYSLPLGLPLLTITWFC 180
|||

QY 175 FCCLRRHQKQNELSDTAGREINLVDHLKSEQTEASTRONSQVLLSEAGIYDNDPDLCLF 234
|||
Db 181 FCCLRRHQKQNELSDTAGREINLVDHLKSEQTEASTRONSQVLLSETGIYDNDPDLCLF 240
|||

QY 235 RMOGSEVSNPCLEENKPGIYVYASLNHSGVGLNSRLARNVKEAPTEYASICVRS 289
|||
Db 241 RMOGSEVSNPCLEENKPGIYVYASLNHSGVGLNSRLARNVKEAPTEYASICVRS 295
|||

RESULT 3
US-10-987-663-8
; Sequence 8, Application US/10987663
; Publication NO. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY L.
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; FILE REFERENCE: P1996R1P1-US
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; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 8
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-8

Query Match 79.6%; Score 1239; DB 6; Length 241;
Best Local Similarity 82.4%; Pred. No. 2.9e-112;
Matches 238; Conservative 1; Mismatches 2; Indels 48; Gaps 1;

QY 1 MKTLPAMLTGKLFVWFVFLIPYLDIWNHSGKSCDVLYIKRQSEHSILAGDPFPELECPV 60
|||
Db 1 MKTLPAMLTGKLFVWFVFLIPYLDIWNHSGKSCDVLYIKRQSEHSILAGDPFPELECPV 60
|||

QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
|||
Db 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANFQ 120
|||

QY 121 SNLIESHTTLYVTVDKASERPSKDEVASRPMWLLYSLPLGLPLLTITWFCCLRR 180
|||
Db 121 SNLIESHTTLYVT-----134

QY 181 HOGKQNELSDTAGREINLVDHLKSEQTEASTRONSQVLLSEAGIYDNDPDLCLFRMORGS 240
|||
Db 135 --GKQNELSDTAGREINLVDHLKSEQTEASTRONSQVLLSETGIYDNDPDLCLFRMORGS 192
|||

QY 241 EYVSNPCLEENKPGIYVYASLNHSGVGLNSRLARNVKEAPTEYASICVRS 289
|||
Db 193 EYVSNPCLEENKPGIYVYASLNHSGVGLNSRLARNVKEAPTEYASICVRS 241
|||

RESULT 4
US-11-183-567A-2
; Sequence 2, Application US/11183567A
; Publication NO. US20060019296A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Ming-Ming
; APPLICANT: Goldfarb, Mitchell
; TITLE OF INVENTION: Methods of Identifying Modulators of the
; FILE REFERENCE: 2459-1-002NCON
; CURRENT APPLICATION NUMBER: US/11/183,567A
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: 09/757,415
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,867
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-567A-2

Query Match 5.8%; Score 90.5; DB 7; Length 822;
Best Local Similarity 21.7%; Pred. No. 0.71;
Matches 69; Conservative 40; Mismatches 116; Indels 93; Gaps 17;

QY 27 NIHGKSCDVLYIKRQSEH-----SILAGDPFPELECPVKYCANRPHVTWCK- 73
|||
Db 234 NEYGSINHTYQLDVVVERSPHRPILOAGLPANETVGSNVFPMCKV-YSDPQPHIQLKH 292
|||

QY 74 --LNG-----TTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCS 116
|||
Db 293 EVVNGSKIGPDNLFPVQILKTAGVNTTKEMEVLHRLNVSP-----EDAGEYTCL 342
|||
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2006, 16:48:30 ; Search time 26.5 Seconds
(without alignments)
1049.307 Million cell updates/sec

Title: US-10-600-997-8

Perfect score: 1557

Sequence: 1 MKTLPAMLTGKLFVWFLLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	7.4	773	1 QRRBG	secretory componen
2	113.5	7.3	841	2 JCS894	killer cell inhibi
3	111	7.1	6642	2 T29757	protein UNC-89 - C
4	110	7.1	335	2 A53434	cell surface glyco
5	107	6.9	1852	2 A37860	calcium channel pr
6	104.5	6.7	1036	2 S22383	axonin 1 precursor
7	104.5	6.7	6805	2 S20901	titin - rabbit (fr
8	104	6.7	7962	2 I38346	elastic titin - hu
9	102.5	6.6	5175	2 T20992	hypothetical prote
10	102.5	6.6	5198	2 T43290	hemectin precurs
11	99.5	6.4	26926	1 I38344	titin, cardiac mus
12	98.5	6.3	480	2 A56182	fibroblast growth
13	98	6.3	1336	2 I60598	Fit-1 tyrosine kin
14	96.5	6.2	1158	2 S33901	reverse transcript
15	94.5	6.1	812	1 A36477	fibroblast growth
16	94	6.0	978	1 A49814	protein-tyrosine k
17	93	6.0	1277	2 T30532	neural cell adhesi
18	92	5.9	3707	2 S18252	heparan sulfate pr
19	91.5	5.9	210	2 S28657	T-cell surface gly
20	91.5	5.9	806	2 A35963	protein-tyrosine k
21	90.5	5.8	480	2 B56182	fibroblast growth
22	90.5	5.8	729	2 A56795	fibroblast growth
23	90.5	5.8	733	2 I49293	fibroblast growth
24	90.5	5.8	822	1 TVWSFG	fibroblast growth
25	90.5	5.8	822	2 I42889	fibroblast growth
26	90.5	5.8	832	2 JH0393	fibroblast growth
27	90.5	5.8	1209	2 T42718	probable neural ce
28	90	5.8	1338	2 S09982	protein-tyrosine k
29	90	5.8	4391	2 A38096	perlecan precursor

30	89.5	5.7	210	2 E46482	T-cell surface gly
31	89.5	5.7	221	2 C46482	T-cell surface gly
32	89.5	5.7	246	2 T01073	T cell surface gly
33	89.5	5.7	296	2 B53434	cell surface glyco
34	89.5	5.7	303	2 A40807	membrane glycoprot
35	89.5	5.7	570	2 A57535	interleukin 1 recep
36	89.5	5.7	814	1 A39752	fibroblast growth
37	89	5.7	214	2 A11073	probable membrane
38	88.5	5.7	192	2 I39464	CD8 antigen - huma
39	88	5.7	244	2 AD1834	isopentenyl transf
40	87.5	5.6	662	2 C40862	heparin-binding gr
41	87.5	5.6	818	2 JC4058	fibroblast growth
42	87.5	5.6	822	1 TVHUF8	fibroblast growth
43	87.5	5.6	822	2 S29840	fibroblast growth
44	87.5	5.6	1177	2 T16594	hypothetical prote
45	87.5	5.6	1323	2 PN0568	connectin 3B - chl

ALIGNMENTS

RESULT 1

QRRBG

secretory component precursor - rabbit

N;Alternate names: poly-Ig receptor; polymeric immunoglobulin receptor

N;Contains: free secretory component; transmembrane secretory component

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004

C;Accession: A02111; A28077

R;Mostov, K.E.; Friedlander, M.; Blobel, G.

Nature 308, 37-43, 1984

A;Title: The receptor for transepithelial transport of IgA and IGM contains multiple ir

A;Reference number: A02111; MUID:84142246; PMID:6322002

A;Accession: A02111

A;Molecule type: mRNA

A;Residues: 1-773 <MOS>

A;Cross-references: UNIPROT:P01832; UNIPARC:UPI0000043E81; GB:X00412; GB:X01291; NID:gi

A;Note: the authors translated the codon ACC for residue 54 as Asn

R;Frutiger, S.; Hughes, G.J.; Hanly, W.C.; Jaton, J.C.

J. Biol. Chem. 263, 8120-8125, 1988

A;Title: Rabbit secretory components of different allotypes vary in their carbohydrate

A;Reference number: A28077; MUID:88228032; PMID:3113339

A;Accession: A28077

A;Molecule type: protein

A;Residues: 87-114;410-424 <FRU>

A;Cross-references: UNIPARC:UPI000017374B; UNIPARC:UPI000017374C

C;Comment: This receptor binds polymeric IgA and IGM at the basolateral surface of epit

C;Comment: cleavage occurs to separate the extracellular portion, also known as the secret

C;Comment: The five domains exhibit homology with immunoglobulin V regions. The similar

C;Comment: Alternative splicing in the extracellular domain leads to high or low molecu

C;Superfamily: secretory component; immunoglobulin homology

C;Keywords: alternative splicing; duplication; glycoprotein; immunoglobulin receptor; p

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-773/Product: transmembrane secretory component #status predicted <MATM>

F;19-575/Product: free secretory component #status predicted <MATP>

F;30-647/Domain: extracellular #status predicted <EXT>

F;39-117/Domain: immunoglobulin homology <IM1>

F;148-227/Domain: immunoglobulin homology <IM2>

F;253-326/Domain: immunoglobulin homology <IM3>

F;362-440/Domain: immunoglobulin homology <IM4>

F;471-540/Domain: immunoglobulin homology <IM5>

F;648-670/Domain: transmembrane #status predicted <TMW>

F;671-773/Domain: intracellular #status predicted <INT>

F;671-115,155-225,260-324,369-438,478-538/Disulfide bonds: #status predicted

F;108/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;418/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 7.4%; Score 115; DB 1; Length 773;

Best Local Similarity 21.2%; Pred. No. 0.064;

Matches 53; Conservative 39; Mismatches 102; Indels 56; Gaps 11;

QY 45 EHSILAGDPFEEC--PVKYCANRPHVTWCKLNGT-TCVKLEDRQTSWKE---EKNISP 97

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 16:43:35 ; Search time 164 Seconds
(without alignments)
1243.279 Million cell updates/sec

Title: US-10-600-997-8
Perfect score: 1557
Sequence: 1 MKTLPMLTGKLFVFFLI.....RLARNVKEAPTEYASICVRS 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1516	97.4	289	1	BTLA_HUMAN	Q7z6a9 homo sapien
2	713.5	45.8	306	1	BTLA_MOUSE	Q7tsa3 mus musculus
3	673.5	43.3	308	1	BTLA_RAT	Q6pm1 rattus norv
4	121.5	7.8	266	1	Q9CUC8_MOUSE	Q9cuc8 mus musculus
5	121.5	7.8	343	1	SLAP1_MOUSE	Q9qum4 mus musculus
6	121.5	7.8	343	2	Q544K1_MOUSE	Q15746 mus musculus
7	117	7.5	1914	1	MYLK_HUMAN	Q15746 homo sapien
8	116	7.5	1914	2	Q5MY99_HUMAN	Q5my99 homo sapien
9	116	7.5	1914	2	Q724J0_HUMAN	Q724j0 homo sapien
10	115	7.4	773	1	PIGR_RABIT	P01832 oryctolagus
11	115	7.4	841	2	Q97484_MOUSE	P97484 mus musculus
12	113.5	7.3	841	2	Q8R2Z1_MOUSE	Q8r2z1 mus musculus
13	111	7.1	5992	2	Q5W615_CABEL	Q5w615 caenorhabdi
14	111	7.1	6632	1	UNC89_CABEL	Q01761 caenorhabdi
15	111	7.1	7122	2	Q5W616_CABEL	Q5w616 caenorhabdi
16	111	7.1	7441	2	Q5W617_CABEL	Q5w617 caenorhabdi
17	111	7.1	8081	2	Q72120_CABEL	Q72120 caenorhabdi
18	110	7.1	335	1	L1RN4_MOUSE	Q64281 mus musculus
19	109	7.0	1026	1	CNTN2_MOUSE	Q62845 rattus norv
20	107	6.9	1272	1	CAC1S_CYPCA	Q5git3 brachydanio
21	107	6.9	1852	1	Q5GIT3_BRARE	P22316 cyprinus ca
22	106	6.8	410	2	Q6R3M2_BOMMO	Q6r3m2 bombyx mori
23	105.5	6.8	841	2	Q54999_MOUSE	Q54999 mus musculus
24	105	6.7	1272	2	Q4JDD5_BRARE	Q4jdd5 brachydanio
25	104.5	6.7	1036	1	CNTN2_CHICK	P28685 gallus gall
26	104.5	6.7	6875	2	Q28733_RABIT	Q28733 oryctolagus
27	104	6.7	410	2	Q6R3M0_BOMMO	Q6r3m0 bombyx mori
28	104	6.7	7562	2	Q10465_HUMAN	Q10465 homo sapien
29	104	6.7	34350	2	Q8WZ42_HUMAN	Q8wz42 homo sapien
30	103.5	6.6	1845	2	Q5MYA0_HUMAN	Q5mya0 homo sapien
31	102.5	6.6	5175	2	Q8I0L3_CABEL	Q8i0l3 caenorhabdi

32	102.5	6.6	5198	2	Q76518_CABEL	Q76518 caenorhabdi
33	102	6.6	326	2	Q8CAU4_MOUSE	Q8cau4 mus musculus
34	102	6.6	428	2	Q6F3J3_MOUSE	Q6f3j3 mus musculus
35	101.5	6.5	1029	2	Q6ZJ63_ORYSA	Q6zj63 oryza sativ
36	101.5	6.5	3410	2	Q7TN00_RAT	Q7tn00 rattus norv
37	101	6.5	5516	2	Q7Z248_BRARE	Q7z248 brachydanio
38	100.5	6.5	410	2	Q7YZA7_BOMMO	Q7yza7 bombyx mori
39	100.5	6.5	410	2	Q4FAT1_BOMMO	Q4fat1 bombyx mori
40	100.5	6.5	4071	2	Q6KDZ1_CHICK	Q6kdz1 gallus gall
41	100	6.4	1561	2	Q924D2_MOUSE	Q924d2 mus musculus
42	100	6.4	1949	2	Q6PDN3_MOUSE	Q6pdn3 mus musculus
43	99.5	6.4	26926	2	Q4UIZ6_HUMAN	Q4uiz6 homo sapien
44	99	6.4	1072	2	Q5VV43_HUMAN	Q5vv43 homo sapien
45	99	6.4	1109	2	Q9Y4G7_HUMAN	Q9y4g7 homo sapien

ALIGNMENTS

RESULT 1
BTLA_HUMAN STANDARD; PRT; 289 AA.
AC Q7Z6A9; Q6ZNH9;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE B and T lymphocyte attenuator precursor (B and T lymphocyte-associated protein).
DE protein).
GN Name=BTLLA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], MUTAGENESIS OF TYR-226; TYR-257 AND
RP TYR-282, N-GLYCOSYLATION, FUNCTION, AND INTERACTIONS WITH PTPN6 AND
RP PTPN11.
RX PubMed=12796776; DOI=10.1038/nj944;
RA Watanabe N., Gavrieli M., Sedy J.R., Yang J., Fallarino F.,
RA Loflin S.H., Hurchla M.A., Zimmerman N., Sim J., Zang X., Murphy T.L.,
RA Russell J.K., Allison J.P., Murphy K.M.;
RA "BTLLA is a lymphocyte inhibitory receptor with similarities to CTLA-4
RT and PD-1".
RL Nat. Immunol. 4:670-679(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 4-289.
RP TISSUE=Trachea;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Shigawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arima M.,
RA Imobe N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Sato T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Negase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.",
 RL Nat. Genet. 36:40-45(2004).
 RN [3].
 RN MUTAGENESIS OF TYR-226; TYR-257 AND TYR-282, AND INTERACTIONS WITH
 RP PTPN6 AND PTPN11.
 RX PubMed=14652006; DOI=10.1016/j.bbrc.2003.11.070;
 RA Gavriel M., Watanabe N., Loftin S.K., Murphy T.L., Murphy K.M.;
 RT "Characterization of phosphotyrosine binding motifs in the cytoplasmic
 RT domain of B and T lymphocyte attenuator required for association with
 RT protein tyrosine phosphatases SHP-1 and SHP-2.",
 RL Biochem. Biophys. Res. Commun. 312:1236-1243(2003).
 RN [4].
 RN INTERACTION WITH TNFRSF14, AND PHOSPHORYLATION.
 RX PubMed=15568026; DOI=10.1038/nrl144;
 RA Sedy J.R., Gavriel M., Potter K.G., Hurchla M.A., Lindsley R.C.,
 RA Hildner K., Scheu S., Pfeiffer K., Ware C.F., Murphy T.L., Murphy K.M.;
 RT "B and T lymphocyte attenuator regulates T cell activation through
 RT interaction with herpesvirus entry mediator.",
 RL Nat. Immunol. 6:90-98(2005).
 CC -!- FUNCTION: Lymphocyte inhibitory receptor which inhibits
 CC lymphocytes during immune response.
 CC -!- SUBUNIT: Interacts with tyrosine phosphatases PTPN6/SHP-1 and
 CC PTPN11/SHP-2. Interacts with TNFRSF14/HVEM.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- PTM: Phosphorylated on Tyr residues by TNFRSF14 and by antigen
 CC receptors crosslinking, both inducing association with PTPN6 and
 CC PTPN11.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AY293286; RAP44003.1; -; mRNA.
 DR EMBL; AK131204; BAD18396.1; ALT INIT; mRNA.
 DR Ensembl; ENSG00000186265; Homo sapiens.
 DR HGNC; HGNC:21087; BTLA.
 DR MIM; 607925; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Glycoprotein; Immune response; Immunoglobulin domain; Phosphorylation;
 KW Receptor; Signal; Transmembrane.
 FT SIGNAL 1 30 Potential.
 FT CHAIN 31 289 B and T lymphocyte attenuator.
 FT TOPO_DOM 31 157 Extracellular (Potential).
 FT TRANSMEM 158 178 Potential.
 FT TOPO_DOM 179 289 Cytoplasmic (Potential).
 FT DOMAIN 13 134 Ig-like V-type.
 FT CARBOHYD 75 75 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT DISULFID 34 63 By similarity.
 FT DISULFID 58 115 By similarity.
 FT MUTAGEN 226 226 Y->F: No change of phosphorylation
 FT implicated in interaction with PTPN6 and
 FT PTPN11. Severe reduction of
 FT phosphorylation;
 FT when associated with F-
 FT 257 and/or F-282.
 FT Y->F: No change of phosphorylation
 FT implicated in interaction with PTPN6 and
 FT PTPN11. Severe reduction of

FT phosphorylation: when associated with F-
 FT 226 and/or F-282.
 FT Y->F: No change of phosphorylation
 FT implicated in interaction with PTPN6 and
 FT PTPN11. Severe reduction of
 FT phosphorylation: when associated with F-
 FT 226 and/or F-257.
 FT V -> M (in Ref. 1).
 FT S -> G (in Ref. 1).
 FT M -> V (in Ref. 1).
 FT C -> W (in Ref. 1).
 FT L -> P (in Ref. 1).
 FT T -> A (in Ref. 1).
 FT Y -> C (in Ref. 1).
 SQ SEQUENCE 289 AA; 32781 MW; 98D1FE325D882642 CRC64;
 Query Match 97.4%; Score 1516; DB 1; Length 289;
 Best Local Similarity 97.9%; Pred. No. 1.5e-123;
 Matches 283; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MKTLPAMLGTKGLFWVFLIPYLDIWNTHGKSCDQVLYIKRQSHSILAGDPFEECPV 60
 DB 1 MKTLPAMLGTKGLFWVFLIPYLDIWNTHGKSCDQVLYIKRQSHSILAGDPFEECPV 60
 QY 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANPQ 120
 DB 61 KYCANRPHVTWCKLNGTTCVKLEDRQTSWKEKNISFFILHPEPMLPNDNGSYRCSANPQ 120
 QY 121 SNLISHSTLYTVTDVKGASRPSKDEVASRPWLLYSLLPLGGLPLLITTWFCFLCCLRR 180
 DB 121 SNLISHSTLYTVTDVKGASRPSKDEVASRPWLLYSLLPLGGLPLLITTWFCFLCCLRR 180
 QY 181 HOGKQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSEAGIYDNDPDLCPFMQSGS 240
 DB 181 HOGKQNELSDTAGREINLVDAHLKSEQTEASTRONSQVLLSEAGIYDNDPDLCPFMQSGS 240
 QY 241 EVCNSPCLLENKPGIVYASLNHSVIGLNSRLARNVKEAPTEYASICVRS 289
 DB 241 EVCNSPCLLENKPGIVYASLNHSVIGLNSRLARNVKEAPTEYASICVRS 289
 RESULT 2
 BTLA_MOUSE
 ID BTLA_MOUSE STANDARD; PRT; 306 AA.
 AC Q7TSA3;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE B and T lymphocyte attenuator precursor (B and T lymphocyte-associated
 DE protein).
 GN Name=BTLA;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Murioidea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), MUTAGENESIS OF TYR-245;
 RP TYR-274 AND TYR-299, N-GLYCOSYLATION, TISSUE SPECIFICITY, INTERACTIONS
 RP WITH PTPN6 AND PTPN11, AND VARIANTS GLU-41; 45-ASN--LYS-47; HIS-52;
 RP TRP-55; GLU-63; TRP-85; GLY-91 AND ARG-102.
 RC STRAIN=129/SVEV;
 RX PubMed=12796776; DOI=10.1038/n1944;
 RA Watanabe N., Gavriel M., Sedy J.R., Yang J.R.,
 RA Loftin S.K., Hurchla M.A., Zimmerman N., Sim J., Zang X., Murphy T.L.,
 RA Russell J.H., Allison J.P., Murphy K.M.;
 RA "BTLA is a lymphocyte inhibitory receptor with similarities to CTLA-4
 RT and PD-1.",
 RL Nat. Immunol. 4:670-679(2003).
 RN [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3), AND VARIANT
 RP THR-143.
 RP STRAIN=C57BL/6J; TISSUE=Thymus;
 RC